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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:32:02 ; Search time 31 Seconds
(without alignments)
158.930 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIVTGTWISYVKNRQ.....KPSBDPWQKACYPGCKYL 66

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	66	2 US-08-511-485-24	Sequence 24, App1
2	386	100.0	66	4 US-09-201-936-24	Sequence 24, App1
3	386	100.0	66	4 US-09-011-356-24	Sequence 24, App1
4	386	100.0	66	4 US-09-201-932-24	Sequence 24, App1
5	386	100.0	496	2 US-08-511-485-10	Sequence 10, App1
6	386	100.0	496	3 US-09-212-971-10	Sequence 10, App1
7	386	100.0	496	3 US-08-800-929A-10	Sequence 10, App1
8	386	100.0	496	3 US-09-617-053A-10	Sequence 10, App1
9	386	100.0	496	4 US-09-201-936-10	Sequence 10, App1
10	386	100.0	496	4 US-09-011-356-10	Sequence 10, App1
11	386	100.0	496	4 US-09-672-717-225	Sequence 225, App1
12	386	100.0	496	4 US-09-201-932-10	Sequence 10, App1
13	386	94.8	66	2 US-08-511-485-25	Sequence 25, App1
14	366	94.8	66	4 US-09-201-936-25	Sequence 25, App1
15	366	94.8	66	4 US-09-011-356-25	Sequence 25, App1
16	366	94.8	66	4 US-09-201-932-25	Sequence 25, App1
17	366	94.8	236	3 US-09-239-867-4	Sequence 4, App1
18	366	94.8	236	4 US-10-024-433-4	Sequence 4, App1
19	366	94.8	497	2 US-08-511-485-4	Sequence 4, App1
20	366	94.8	497	3 US-09-212-971-4	Sequence 4, App1
21	366	94.8	497	3 US-08-800-929A-4	Sequence 4, App1
22	366	94.8	497	3 US-09-617-053A-4	Sequence 4, App1
23	366	94.8	497	4 US-08-657-759-2	Sequence 2, App1
24	366	94.8	497	4 US-09-201-936-4	Sequence 4, App1
25	366	94.8	497	4 US-09-011-356-4	Sequence 4, App1
26	366	94.8	497	4 US-09-672-717-219	Sequence 219, App1
27	366	94.8	497	4 US-09-201-932-4	Sequence 4, App1

28	366	94.8	497	4 US-09-949-016-6032	Sequence 6032, App1
29	334	86.5	236	3 US-09-121-979-4	Sequence 4, App1
30	334	86.5	236	3 US-09-332-319-4	Sequence 4, App1
31	334	86.5	236	3 US-09-239-867-2	Sequence 2, App1
32	334	86.5	236	4 US-10-024-433-2	Sequence 2, App1
33	279	72.3	53	4 US-08-657-759-19	Sequence 19, App1
34	233	60.4	50	3 US-08-975-080-28	Sequence 28, App1
35	233	60.4	50	3 US-08-975-080-29	Sequence 28, App1
36	233	60.4	50	3 US-08-975-080-32	Sequence 28, App1
37	233	60.4	50	4 US-10-138-618-28	Sequence 28, App1
38	233	60.4	50	4 US-10-138-618-29	Sequence 28, App1
39	233	60.4	50	4 US-10-138-618-32	Sequence 28, App1
40	198	51.3	68	2 US-08-511-485-26	Sequence 26, App1
41	198	51.3	68	4 US-09-201-936-26	Sequence 26, App1
42	198	51.3	68	4 US-09-011-356-26	Sequence 26, App1
43	198	51.3	68	4 US-09-201-932-26	Sequence 26, App1
44	198	51.3	442	4 US-09-579-6928-58	Sequence 58, App1
45	198	51.3	604	2 US-08-511-485-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-08-511-485-24
Sequence 24, Application US/08511485
Patent No. 591912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-24

Query Match 100.0%; Score 386; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4,1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIVTGTWISYVKNRQALAGPVALBGDKYKCFHCGGGLTDKPKPSBDPWQKACYPGCKYL 60
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Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60
QY 61 PGCKYL 66
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Db 61 PGCKYL 66

RESULT 2
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60
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Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60

QY 61 PGCKYL 66
| | | | |
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60
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Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60

QY 61 PGCKYL 66
| | | | |
Db 61 PGCKYL 66

RESULT 4
US-09-201-932-24
; Sequence 24, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-24

Query Match 100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60
| | | | |
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAKCY 60

QY 61 PGCKYL 66
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Db 61 PGCKYL 66

RESULT 5
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/08/511,485
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-10

Query Match 100.0%; Score 386; DB 2; Length 496;

Best Local Similarity 100.0%; Pred. No. 4,7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 264 YEARIYFGTWISVKNKQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
US-09-212-971-10
Sequence 10, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT

ORGANISM: Mus musculus
US-09-212-971-10

Query Match 100.0%; Score 386; DB 3; Length 496;

Best Local Similarity 100.0%; Pred. No. 4,7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIYFGTWISVKNKQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 264 YEARIYFGTWISVKNKQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKCY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
US-08-800-929A-10

Sequence 10, Application US/08800929A
Patent No. 6133437

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF

TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Beker-Brady, Kristina

REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-10

Query Match 100.0%; Score 386; DB 3; Length 496;

Best Local Similarity 100.0%; Pred. No. 4,7e-42; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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RESULT 8
US-09-617-053A-10
; Sequence 10: Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Charlene
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-617-053A-10

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	Query Match	100.0%;	Score 386;	DB 3;	Length 496;
	Best Local Similarity	100.0%;	Pred. No. 4.7e-42;		
Matches	66; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0
OY	1 YEARIVTGTWISYNKEQLARAGFYALGEGDVKVCFPHGGGLTDWKPSDEPDHAKCY	60			
Dy	264 YEARIIVTFGTWIYSVNKQELAPRAGFYALGEGDVKKFCFHGGGLTDWKPSDEPDHAKCY	323			
OY	61 PGCKYL 66 				
Dy	324 PGCKYL 329				

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RESULT 9
US-09-201-936-10
; Sequence 10, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneljuk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FaastSeq for Windows Version 3.0

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; SEQ ID NO 10
; LENGTH: 496
; TYPE: prt
; ORGANISM: Mus musculus
US-09-201-936-10

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Query Match	100.0%;	Score 386;	DB 4;	length 496;
Best Local Similarity	100.0%;	Pred. No. 4.7e-42;		
Matches 66;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	YEARITVFGWIIYSVNKEQLAPAGFYALGEGDKVCFFHCGGGLTDNKRSEBDMQHAKCY	60
Dd	264	YEARIVTFGMWIYSVNKEQLARAGFYALGEGDKVCFFHCGGGLTDMKRSBEDPMQDHAKCY	322
QY	61	PGCKYL	66
Dd	324	PGCKYL	329

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RESULT 10
US-09-011-356-10
; Sequence 10. Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; TITLE OF INVENTION: PROBES AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRN
; ORGANISM: Mus musculus
; US-09-011-356-10

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Query Match	100.0%;	Score 386;	DB 4;	Length 496;
Best Local Similarity	100.0%;	Pred. No. 4.7e-42;		
Matches 66;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	YEARITFTFTWTVSYVNKEQLARAGFYALGEBDDKYKCFHCGGGLTDMKPSBEPMDHAKCY	60
Db	264	YEARITFTFTWTVSYVNKEQLARAGFYALGEBDDKYKCFHCGGGLTDMKPSBEPMDHAKCY	323
QY	61	PGCKTLL	66
Db	324	PGCKTLL	329

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RESULT 11
US-09-672-717-225
; Sequence 225, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Theretool
; FILE REFERENCE: 07891/025001

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; CURRENT APPLICATION NUMBER: US/09/672,717
 ; CURRENT FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 225
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-672-717-225

Query Match 100.0%; Score 386; DB 4; Length 496;
 Best Local Similarity 100.0%; Pred. No. 4,7e-42;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 60
 DB 264 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 12
 US-09-201-932-10
 ; Sequence 10, Application US/09201932A
 ; Patent No. 6689562
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003004
 ; CURRENT APPLICATION NUMBER: US/09/201,932A
 ; CURRENT FILING DATE: 1998-12-01
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-201-932-10

Query Match 100.0%; Score 386; DB 4; Length 496;
 Best Local Similarity 100.0%; Pred. No. 4,7e-42;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 60
 DB 264 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329

RESULT 13
 US-08-511-485-25
 ; Sequence 25, Application US/08511485
 ; Patent No. 5919912
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/511,485
 ; FILING DATE: 04-AUG-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 07540/002001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 66 amino acid
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: both
 ; MOLECULE TYPE: protein
 US-08-511-485-25

Query Match 94.8%; Score 366; DB 2; Length 66;
 Best Local Similarity 95.5%; Pred. No. 1,7e-40;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 60
 DB 1 YEARIVFGTWISVNEKQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAACY 60
 QY 61 PGCKYL 66
 DB 61 PGCKYL 66

RESULT 14
 US-09-201-936-25
 ; Sequence 25, Application US/09201936
 ; Patent No. 6541457
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; CURRENT FILING DATE: 1998-12-01
 ; EARLIER APPLICATION NUMBER: 09/011,356
 ; EARLIER FILING DATE: 1998-02-04
 ; EARLIER APPLICATION NUMBER: PCT/IB96/01022
 ; EARLIER FILING DATE: 1996-08-05
 ; EARLIER APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.7e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 15
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011.356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.7e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 16
US-09-201-932-25
; Sequence 25, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004

; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.7e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 60

QY 61 PGCKYL 66
|||
Db 61 PGCKYL 66

RESULT 17
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 94.8%; Score 366; DB 3; Length 236;
Best Local Similarity 95.5%; Pred. No. 7.9e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
|||
Db 4 YEARIVTGTWIVSYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMY 63

QY 61 PGCKYL 66
|||
Db 64 PGCKYL 69

RESULT 18
US-10-024-433-4
; Sequence 4, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:

; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: MALE FERTILITY

```
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/10/024,433
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/239,867
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-433-4

Query Match          94.8%; Score 366; DB 4; Length 236;
Best Local Similarity 95.5%; Pred. No. 7.9e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
   |||||
DB 4 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 63

QY 61 PGCKYL 66
   |||||
DB 64 PGCKYL 69

RESULT 19
US-08-511-485-4
Sequence 4, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-4

Query Match          94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
   |||||
DB 265 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
   |||||
DB 325 PGCKYL 330

RESULT 20
US-09-212-971-4
Sequence 4, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
NUMBER OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-4

Query Match          94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
   |||||
DB 265 YEARIYFTGWIYVYNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
   |||||
DB 325 PGCKYL 330

RESULT 21
US-08-800-929A-4
Sequence 4, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
NUMBER OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
```

```

; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-4

Query Match
Best Local Similarity 94.8%; Score 366; DB 3; Length 497;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 22
US-09-617-053A-4
; Sequence 4, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-617-053A-4
```

```

Query Match
Best Local Similarity 94.8%; Score 366; DB 3; Length 497;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 23
US-08-657-759-2
; Sequence 2, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Duckett, Colin S.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-657-759-2

Query Match
Best Local Similarity 94.8%; Score 366; DB 4; Length 497;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTWYSVNKEQLARAGFYALGSGDKVCKFCGCGGLTDMKPSDPMDOHAKMY 324
QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 24
US-09-201-936-4
; Sequence 4, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
```

```

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324

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```

QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 25
US-09-011-356-4
; Sequence 4, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324

```

```

QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 26
US-09-672-717-219
; Sequence 219, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-672-717-219

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```

Query Match          94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 60
DB 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMQHAQKY 324

```

```

QY 61 PGCKYL 66
DB 325 PGCKYL 330

```

```

RESULT 27
US-09-201-932-4
; Sequence 4, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-4

```

```

Query Match          94.8%; Score 366; DB 4; Length 497;

```

```
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 28
US-09-949-016-6032
; Sequence 6032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6032
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6032

Query Match 94.8%; Score 366; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.9e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 29
US-09-121-979-4
; Sequence 4, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-979-4

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
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QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 60
Db 4 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 30
US-09-332-319-4
; Sequence 4, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-332-319-4

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 60
Db 4 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 31
US-09-239-867-2
; Sequence 2, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-2

Query Match 86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.2e-35;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 60
Db 4 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQHAACY 63
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QY	61	PGCKYL	66
Db	64	PGCKYL	69

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RESULT 32
US-10-024-433-2
; Sequence 2, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024.433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-433-2

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QY 1 YEAR:VTFPGWITSVNNQGLARAGFYALGSGDKYKCFHCGGSLTDWKPSESDPMDQAHXCY 63
 Db 4 YEAR:LITFGWMTSVNNQGLARAGFYALGSGDKYKCFHCGGSLTDWKPSESDPMDQAHXCY 63
 QY 61 PGCKYL 66
 Db 64 PGCKYL 69
 RESULT 33
 US-08-657-759-19
 Sequence 19, Application US/08657759
 Patent No. 6511828
 GENERAL INFORMATION:
 APPLICANT: Thompson, Craig B.
 APPLICANT: Duckett, Colin S.
 TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
 TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,759
 FILING DATE: 31-MAY-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: ARCD:220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577

```

; INFORMATION FOR SEQ ID NO: 19
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 53 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;
US-08-657-759-19

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Query Match	72.3%;	Score 279;	DB 4;	Length 53;
Best Local Similarity	-95.9%;	Pred. No. 3.1e-29;		
Matches 47; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

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RESULT 34
US-08-975-080-28
: Sequence 28, Application US/08975080
: Patent No. 6245523
: GENERAL INFORMATION:
: APPLICANT: Altieri, Dario C.
: TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
: TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
: STREET: 1800 M Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036-5869
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/975,080
: FILING DATE: 20-NOV-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/031,435
: FILING DATE: 20-NOV-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Adler, Reid G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-467-7000
: TELEFAX: 202-467-7176
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 50 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MODECLUTYPE: protein
: US-08-975-080-28

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 27 ALHGDKVYKCFHCGGGLTDWKPSPDPDQNAKCYPGCKYL 66
Db 1 ALHGDKVYKCFHCGGGLTDWKPSPDPDQNAKWPYGGCKYL 40

```

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 60/031,435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-29

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTWKPSDEPDWDHAKCYPGCKYL 66
DB 1 ALGEGDKVKCFHCGGGLTWKPSDEPDWDHAKCYPGCKYL 40

RESULT 36
US-08-975-080-32
Sequence 32, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-32

Query Match 60.4%; Score 233; DB 3; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTWKPSDEPDWDHAKCYPGCKYL 66
DB 1 ALGEGDKVKCFHCGGGLTWKPSDEPDWDHAKCYPGCKYL 40

RESULT 37
US-10-138-618-28
Sequence 28, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 40

RESULT 38
US-10-138-618-29
Sequence 29, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 40

RESULT 39
US-10-138-618-32
Sequence 32, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match 60.4%; Score 233; DB 4; Length 50;
Best Local Similarity 95.0%; Pred. No. 3e-23;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDMKPSSEDPWDQAKCYPGCKYL 40

RESULT 40
US-08-511-485-26
Sequence 26, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514

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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:18:26 ; Search time 115 Seconds
(without alignments)
221.967 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYVFTGWTIVSVNKEQL.....KPSHPDWDHAKCYGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	386	100.0	496	2	AAW19584 Mouse apo
2	386	100.0	496	2	AAW69297 Murine XI
3	386	100.0	496	5	ABG65666 Mouse inh
4	372	96.4	66	7	ADB61828 Mouse inh
5	372	96.4	496	6	ABP72157 Mouse inh
6	366	94.8	66	7	ADB61827 Rat inh
7	366	94.8	66	7	ADB61810 Human inh
8	366	94.8	110	8	ADP90805 Human XIA
9	366	94.8	236	5	ABG32418 X-linked
10	366	94.8	278	5	AAO20511 Protein o
11	366	94.8	497	2	AAW19581 Human apo
12	366	94.8	497	2	AAW69294 Human XIA
13	366	94.8	497	3	AAV59451 Human XIA
14	366	94.8	497	3	AAV99985 Human X-1
15	366	94.8	497	5	ABG65663 Human inh
16	366	94.8	497	7	ADB80961 RING-SH c
17	366	94.8	497	7	ADI39804 Human inh
18	366	94.8	497	8	ADH74639 Human XIA
19	366	94.8	497	8	ADL70166 Human X c
20	366	94.8	497	8	ADP23982 PRO polyp
21	357	92.5	496	2	AAW19745 Mouse inh
22	357	92.5	66	7	ADB61820 Human inh
23	334	86.5	236	3	AAV81440 Human TIA
24	334	86.5	236	4	AAE00365 Human TAP
25	334	86.5	236	5	AAU75066 Human tes

26	334	86.5	236	5	ABG32417	ABG32417 Inhibitor
27	334	86.5	464	5	AAU75747	AAU75747 Human inh
28	328	85.0	236	4	AAE00366	AAE00366 Chimpanzee
29	326.5	84.6	87	8	ADR44576	ADR44576 X-IAP BIR
30	325	84.2	66	7	ADB61831	ADB61831 Gorilla i
31	325	84.2	236	4	AAE00367	AAE00367 Gorilla i
32	306	79.3	57	7	ADB61832	ADB61832 Unidentif
33	279	72.3	53	7	ADI39821	ADI39821 Human NAI
34	279	72.3	66	7	ADB61829	ADB61829 Chicken i
35	260	67.4	151	5	ADK34975	ADK34975 Novel hum
36	258	66.8	52	7	ADB61830	ADB61830 Bovine in
37	212	54.9	68	7	ADB61833	ADB61833 Zebra fib
38	198	51.3	68	7	ADB61813	ADB61813 Human inh
39	198	51.3	442	8	ADO26592	ADO26592 Human API
40	198	51.3	557	6	ABP72159	ABP72159 Inhibitor
41	198	51.3	604	2	AAW19582	AAW19582 Human apo
42	198	51.3	604	2	AAW19747	AAW19747 Human inh
43	198	51.3	604	2	AAW13546	AAW13546 Human C-I
44	198	51.3	604	2	AAW69295	AAW69295 Human HIA
45	198	51.3	604	2	AAV52703	AAV52703 Human cel

ALIGNMENTS

RESULT 1	AAW19584	standard; protein; 496 AA.
ID	AAW19584	
XX	AAW19584;	
AC		
XX		
DT	02-SEP-1997	(first entry)
XX		
DE	Mouse apoptosis inhibitor M-XIAP.	
XX		
KW	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;	
KW	HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;	
KW	myocardial infarction; stroke; reperfusion injury;	
KW	tox-in-induced liver disease; gene therapy; diagnosis.	
XX		
OS	Mus sp.	
XX		
PH	Key	Location/Qualifiers
FT	Domain	26..93
FT	Domain	/label= BIR-1
FT	Domain	163..230
FT	Domain	/label= BIR-2
FT	Domain	264..329
FT	Domain	/label= BIR-3
FT	Domain	438..483
FT	Domain	/label= Ring_zinc_finger
XX		
XX	W09706255-A2.	
XX		
PD	20-FEB-1997.	
XX		
PE	05-AUG-1996;	96WO-IB001022.
XX		
PR	04-AUG-1995;	95US-00511485.
PR	22-DEC-1995;	95US-00576956.
XX		
PA	(UYOT-) UNIV OTTAWA.	
PI		
XX	korneluk RG, Mackenzie AE, Baird S, Liston P;	
XX		
DR	WPI; 1997-154262/14.	
DR	N-PSDB; AAT70839.	
XX		
PT	Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to	
PT	inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of	
PT	suceptibility to apoptotic disease.	
XX		
PS	Claim 27; Page 79-80; 219pp; English.	

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
 CC was deduced from the m-xiap gene (AA170839) isolated from a mouse embryo
 CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
 CC vitro or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 XX
 SQ Sequence 496 AA;
 Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYVYNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFGTWIYVYNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329
 RESULT 2
 AAW69297
 ID AAW69297 standard; protein; 496 AA.
 AC AAW69297;
 XX 13-NOV-1998 (first entry)
 DT
 XX
 DE Murine XIAP protein.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KM proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
 XX
 OS Mus sp.
 XX
 PN WO9835693-A2.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-IB000781.
 XX
 PR 13-FEB-1997; 97US-00800929.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 XX
 DR WPI, 1998-467164/40.
 DR N-PSDB; AAV55041.
 XX
 XX
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
 PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX
 PS Disclosure; Fig 4; 147p; English.
 XX
 XX This sequence is the murine XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 XX
 SQ Sequence 496 AA;
 Query Match 100.0%; Score 386; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYVYNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 60
 DB 264 YEARIYFGTWIYVYNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPMDOHAKCY 323
 QY 61 PGCKYL 66
 DB 324 PGCKYL 329
 RESULT 3
 ABG65666
 ID ABG65666 standard; protein; 496 AA.
 AC ABG65666;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Mouse inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; antisense; inhibitor of apoptosis; HIAP1, HIAP2, XIAP; cytostatic;
 KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KM embryonic development; viral pathogenesis; autoimmune disorder;
 KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KM herpes virus infection; pox virus infection; adenovirus infection;
 KM proliferative disease.
 XX
 OS Mus sp.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PA (AECE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI, 2002-479562/51.
 DR N-PSDB; ABK93872.
 XX
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX
 PS Example 12; Fig 4; 135p; English.
 XX
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 386; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 2e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIYFGTWIYSVNNKQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHKCY 60
DB 264 YEARIYFGTWIYSVNNKQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHKCY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329
RESULT 4
ADB61828
ID ADB61828 standard; protein; 66 AA.
AC ADB61828;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM H1AP1; cIAP2; H1AP2; cIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytostatic; neoplasm; leukemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms' tumour; BIR 3 domain; mouse; murine.
XX
OS Mus sp.
PN MO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002MO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
PR 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
PI Boudreault A, Korneluk RG, La Casse E, Liston P;
DR WPI; 2003-513532/48.
XX
PT Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, H1AP1
CC (cIAP2) and H1AP2 (cIAP1) all possess three BIR domains and a carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.
XX
SQ Sequence 66 AA;
Query Match 96.4%; Score 372; DB 7; Length 66;
Best Local Similarity 97.0%; Pred. No. 1.1e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIYFGTWIYSVNNKQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHKCY 60
DB 1 YEARIYFGTWIYSVNNKQLARAGFYALGEGDKVCKFCGCGGLTDMKPSBDPMDQHKCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66
RESULT 5
ABP72157
ID ABP72157 standard; protein; 496 AA.
AC ABP72157;
XX
DT 22-APR-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis protein MIAP3.
XX
KM Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukemia;
KM lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
XX
OS Mus sp.
PN MO2003004606-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002MO-US021002.
XX
PR 03-JUL-2001; 2001US-00898158.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
PI Troy CM, Shelanski ML;
DR WPI; 2003-210351/20.
DR N-PSDB; ABZ58102.
XX
PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
PT treating cancer, neurodegenerative disorder or cardiomyopathy.
XX
PS Disclosure; Fig 15A; 124pp; English.
XX
CC The present sequence is the protein sequence of murine inhibitor of
CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as

CC an antisense oligonucleotide, which specifically hybridises to a nucleic
CC acid encoding an inhibitor of apoptosis protein, especially XIAP1, XIAP2,
CC XIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
CC death comprises contacting the cell with the nucleic acid under
CC conditions permitting the nucleic acid to enter the cell, especially the
CC use of a vector, liposome, or a mechanical or electrical means. The
CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
CC cell carcinoma and squamous cell carcinoma (all claimed)
SQ Sequence 496 AA;

Query Match 96.4%; Score 372; DB 6; Length 496;
Best Local Similarity 97.0%; Pred. No. 1.1e-37;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDDPMQDAKCY 60
DB 264 YEARIYFTGWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDDPMQDAKCY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 6
ADB61827 standard; protein; 66 AA.
ADB61827:
04-DEC-2003 (first entry)
DE Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM HIAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms' tumour; BIR 3 domain; rat.
XX Rattus sp.
XX WO2003040172-A2.
XX 15-MAY-2003.
XX 12-NOV-2002; 2002MO-CA001738.
XX 09-NOV-2001; 2001US-0332300P.
XX 08-APR-2002; 2002US-0370934P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Boudreault A, Korneluk RG, La Casse E, Liston P;
XX WPI, 2003-513532/48.
XX
XX Polypeptide capable of forming a complex with a polypeptide comprising a
XX baculovirus inhibitor of apoptosis repeat domain useful for treating a
XX cancer and other neoplasms.
XX
XX Disclosure, Fig 1B; 53pp; English.
XX
XX This invention relates to a substantially pure polypeptide having a
XX length of less than 100 amino acids and capable of forming a complex with
XX a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
CC that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.
SQ Sequence 66 AA;

Query Match 94.8%; Score 366; DB 7; Length 66;
Best Local Similarity 93.9%; Pred. No. 6.1e-38;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDDPMQDAKCY 60
DB 1 YDARIYFTGWISVVKKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDDPMQDAKCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 7
ADB61810 standard; protein; 66 AA.
ADB61810:
04-DEC-2003 (first entry)
DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM HIAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms' tumour; human; BIR 3 domain.
XX Homo sapiens.
XX WO2003040172-A2.
XX 15-MAY-2003.
XX 12-NOV-2002; 2002MO-CA001738.
XX 09-NOV-2001; 2001US-0332300P.
XX 08-APR-2002; 2002US-0370934P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Boudreault A, Korneluk RG, La Casse E, Liston P;
XX

DR WPI; 2003-513532/48.
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1A; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HAPI2 (CIAP1) all possess three BIR domains and caspase
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC against which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 66 AA;
 QY
 Query Match 94.8%; Score 366; DB 7; Length 66;
 Best Local Similarity 95.5%; Pred. No. 6.1e-38;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHAKEY 60
 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHAKEY 60
 QY 61 PGCKYL 66
 61 PGCKYL 66
 Db 61 PGCKYL 66
 RESULT 8
 ADP90805
 ID ADP90805 standard; peptide; 110 AA.
 XX
 AC ADP90805;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human XIAP protein BIR-3 domain.
 XX
 KW protein labelling; peptide labelling;
 KW irreversible affinity tagging residue;
 KW reversible affinity tagging residue; high throughput screening assay;
 KW pharmaceutical agent; human; XIAP; BIR-3.
 XX
 OS Homo sapiens.
 XX
 PN WO2004051270-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 04-DEC-2003; 2003WO-EP013715.
 XX
 PR 05-DEC-2002; 2002GB-00028429.
 XX
 PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.
 XX
 PI Auer M, Meisner N, Seifert J;
 XX
 DR WPI; 2004-480677/45.
 XX
 PT Providing labeled target protein or target peptide by contacting chemical
 PT compound with affinity support, removing impurities in reaction mixture
 PT surrounding affinity support, cleaving or eluting chemical molecule from
 PT affinity support.
 XX
 PS Example 6; Page 46; 81pp; English.
 XX
 CC The invention comprises a method for providing a labelled target
 CC protein/peptide. The method involves contacting a chemical compound with
 CC affinity support, removing impurities in the reaction mixture surrounding
 CC the affinity support to which the chemical molecule is bound, and
 CC cleaving or eluting the molecule from the affinity support to obtain
 CC irreversible or reversible affinity tagging residue, labelled target
 CC protein or labelled peptide. The method of the invention is useful for
 CC labelling a target protein/peptide or high throughput screening assay.
 CC The method of the invention is useful for identifying agents that
 CC modulate the activity or characteristics of a target protein/peptide -
 CC such agents are useful as pharmaceuticals. The present amino acid
 CC sequence represents the BIR-3 domain from the human XIAP protein which
 CC was used in an example of the invention.
 XX
 SQ Sequence 110 AA;
 QY
 Query Match 94.8%; Score 366; DB 8; Length 110;
 Best Local Similarity 95.5%; Pred. No. 1.1e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 17 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHAKEY 60
 17 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHAKEY 76
 QY 61 PGCKYL 66
 61 PGCKYL 66
 Db 77 PGCKYL 82
 RESULT 9
 ABG32418
 ID ABG32418 standard; protein; 236 AA.
 XX
 AC ABG32418;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE X-linked inhibitor of apoptosis protein, XIAP.
 XX
 KW Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
 KW fertility; testicular cancer; male infertility; male birth control;
 KW X-linked inhibitor of apoptosis protein; XIAP.
 XX
 OS Mammalia.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note="Encoded by nnn; start codon is illegible in
 FT specification"
 XX
 PN US2002086409-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 18-DEC-2001; 2001US-00024433.
 XX
 PR 29-JAN-1998; 98US-0073001P.
 PR 29-JAN-1999; 99US-00239867.
 XX
 PA (KORN/) KORNELUK R G.

PA (UYOT-) UNIV OTTAWA.
 XX Korneljuk RG, Mackenzie AB, Baird S, Liston P;
 XX WPI; 1997-154262/14.
 DR N-PSDB; AAT70836.
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
 PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
 PT susceptibility to apoptotic disease.
 XX Claim 27; Page 68-70; 219pp; English.
 PS Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
 CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
 CC of apoptosis (IAP) and which are characterised by the presence of a ring
 CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
 CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
 CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
 CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
 CC or in vivo) and used in methods for treating diseases and disorders
 CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
 CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
 CC an ischaemic injury, selected from myocardial infarction, stroke,
 CC reperfusion injury, or a toxin-induced liver disease
 CC
 SQ Sequence 497 AA;
 Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 60
 Db 265 YEARIFFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330
 RESULT 12
 AAW69294 ID AAW69294 standard; protein; 497 AA.
 XX AAW69294;
 XX 13-NOV-1998 (first entry)
 XX Human XIAP protein.
 DE Human XIAP protein.
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KM proliferative disease; IAP; therapy; cancer; human; XIAP protein.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO9835693-A2.
 PD 20-AUG-1998.
 PF 13-FEB-1998; 98WO-IB000781.
 PR 13-FEB-1997; 97US-00800929.
 XX (UYOT-) UNIV OTTAWA.
 PI Korneljuk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
 DR WPI; 1998-467164/40.
 DR N-PSDB; AAV55038.
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
 PT or NAIP polypeptide - also methods for prognosis based on presence of IAP

PT and NAIP, specifically applied to cancers involving p53 mutations.
 XX Disclosure; Fig 1; 147pp; English.
 XX This sequence is the human XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors
 SQ Sequence 497 AA;
 Query Match 94.8%; Score 366; DB 2; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIVFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 60
 Db 265 YEARIFFGTWIYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQHKY 324
 QY 61 PGCKYL 66
 Db 325 PGCKYL 330
 RESULT 13
 AAY59451 ID AAY59451 standard; protein; 497 AA.
 XX AAY59451;
 XX 24-MAR-2000 (first entry)
 XX Human XIAP protein sequence.
 DE Human XIAP protein sequence.
 XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KM transforming growth factor-beta activated kinase 1; monocyte migration;
 KM TAK1 binding protein 1; extracellular matrix protein production;
 KM cell growth inhibitor; beta-amyloid protein deposition;
 KM immunosuppression; Transforming growth factor-beta.
 XX Homo sapiens.
 OS Homo sapiens.
 PN JP1326328-A.
 PD 26-NOV-1999.
 PF 13-MAY-1998; 98JP-00130378.
 PR 13-MAY-1998; 98JP-00130378.
 XX (MATS/) MATSUMOTO K.
 PA WPI; 2000-078337/07.
 DR N-PSDB; AA248862.
 XX Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein.
 PS Claim 3; Page 28-30; 43pp; Japanese.
 CC This sequence represents the human XIAP protein. The invention relates to
 CC a method for screening a substance inhibiting the formation of a complex

CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug

XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 6,4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCHCGGLTDWKPSEDPMDQAKCY 60
DB 265 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCHCGGLTDWKPSEDPMDQAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 14
AAV9985
ID AAV9985 standard; protein; 497 AA.

XX
AC AAV9985;

XX
DT 07-NOV-2000 (first entry)

XX
DE Human X-linked inhibitor of apoptosis.

XX
KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880; antisense;
KW antiinflammatory; cytostatic; tumour.

XX
OS Homo sapiens.

XX
PN US6087173-A.

XX
PD 11-JUL-2000.

XX
PF 09-SEP-1999; 99US-00392580.

XX
PR 09-SEP-1999; 99US-00392580.

XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Bennett CF, Cowser LM, Ackermann EJ;

XX
DR WPI: 2000-498201/44.

XX
DR N-PSDB; AAA64901.

PT Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

XX
PS Example 13; Col 43-48, 33pp; English.

XX
XX The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis (the
CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
CC more effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
CC expression in cells and tissues in vitro. The oligonucleotides are also
CC useful for treating animals or humans, prone to a disease associated with
CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
CC prophylactically to prevent infection, inflammation or tumour formation

SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 6,4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCHCGGLTDWKPSEDPMDQAKCY 60
DB 265 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCHCGGLTDWKPSEDPMDQAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 15
ABG65663
ID ABG65663 standard; protein; 497 AA.

XX
AC ABG65663;

XX
DT 26-AUG-2002 (first entry)

XX
DE Human inhibitor of apoptosis, XIAP.

XX
KW Human; antisense; inhibitor of apoptosis; HIAPI; HIAPI2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.

XX
OS Homo sapiens.

XX
PN W0200226968-A2.

XX
PD 04-APR-2002.

XX
PF 27-SEP-2001; 2001WO-CA001379.

XX
PR 28-SEP-2000; 2000US-00672717.

XX
PA (UYOT-) UNIV OTTAWA.

XX
PI (ABGE-) AEGERA THERAPEUTICS INC.

XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX
DR WPI: 2002-479562/51.

XX
DR N-PSDB; ABR93869.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.

XX
PS Example 12; Fig 1; 135pp; English.

XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAPI or HIAPI2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP

CC protein sequence
XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 5; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 16
ADB80961
ID ADB80961 standard; protein; 497 AA.

AC ADB80961;

DT 04-DEC-2003 (first entry)

DE RING-SH complex related protein, SEQ ID No 35.

XX RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hep60;
KM Hep70; Hep90; STAM1; STAM2A; STAM2B; VHS-UTM; GTPase; E2 enzyme; csg101;
KM cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KM rhadovirus; filovirus.

XX Undifferentiated.

OS W0203033646-A2.

PN 24-APR-2003.

PF 31-JUL-2002; 2002MO-US024589.

PR 31-JUL-2001; 2001US-0308958P.

PR 09-NOV-2001; 2001US-0345846P.

PA (PROT-) PROTEOLOGICS INC.

PI Greener T, Moskowitz H, Reis Y, Alroy I;

DR WPI; 2003-393509/37.

DR N-PSDB; ADB81002.

XX New isolated protein complex comprising a RING-SH 3 polypeptide and
PT another polypeptide, useful for detecting cells infected with a virus,
PT and for treating viral disorders caused by retroviruses, rhadoviruses,
PT or filoviruses.

PS Disclosure; Fig 35; 176pp; English.

XX The invention relates to a novel isolated protein complex comprising a
CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC Gag late domain, PI3K, actin, myosin, Hep60, Hep70, Hep90, STAM1, STAM2A,
CC STAM2B, VHS-UTM, a GTPase, an E2 enzyme, csg101, a cullin, RING-SH, and a
CC clathrin. The novel protein complex has virucide activity and can be used
CC to treat disorders as part of a vaccine. The protein complex and
CC composition are useful for detecting cells infected with a virus, for
CC identifying agents having antiviral activity, and for treating viral
CC disorders caused by retroviruses, rhadoviruses, or filoviruses. This
CC sequence is a protein comprising the RING-SH complex of the invention.

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 7; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 17
AD139804
ID AD139804 standard; protein; 497 AA.

AC AD139804;

DT 15-APR-2004 (first entry)

DE Human inhibitor of apoptosis-like protein (ilp).

XX Inhibitor of apoptosis-like protein; ilp; apoptosis; therapy;
KM cancer; cell immortalisation; cysteine protease; viral infection;
KM cytosolic; virucide; human.

XX Homo sapiens.

OS US6511828-B1.

PN 28-JAN-2003.

PF 31-MAY-1996; 96US-00657759.

PR 31-MAY-1996; 96US-00657759.

PA (ARCH-) ARCH DEV CORP.

PI Thompson CB, Duckett CS;

DR WPI; 2003-391256/37.

XX New inhibitor of apoptosis-like protein (ilp) and polynucleotide encoding
PT ilp, useful for inhibiting or stimulating apoptosis in target cells,
PT treating certain cancers, or sustaining host cell survival following
PT viral infection.

PS Claim 1; SEQ ID NO 2; 42pp; English.

XX The present invention relates to inhibitor of apoptosis (iap)-like
CC proteins (ilp) and polynucleotides encoding such proteins. Sequences of
CC the invention are useful for inhibiting or stimulating apoptosis in
CC target cells or for treating certain cancers. They are also useful in the
CC immortalisation of cells for culture, for inhibiting the activation of
CC cysteine proteases and to sustain host cell survival following viral
CC infection. The ilp may also be used as a marker in gel separation
CC procedures or as a standard in protein concentration determinations. The
CC present sequence is human inhibitor of apoptosis-like protein.

XX Sequence 497 AA;

Query Match 94.8%; Score 366; DB 7; Length 497;
Best Local Similarity 95.5%; Pred. No. 6.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 265 YEARIYFTGWTIYVSNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKMY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 18

KW osteopathic; antidiabetic; dermatological; antipsoriatic; anti-allergic;
 KM antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;
 PI Mu TD;
 XX WPI; 2004-419628/39.
 DR N-PSDB; ADP23981.
 XX
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 1160; 2940bp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiallergic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, anti-allergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 497 AA;
 XX
 Query Match 94.8%; Score 366; DB 8; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.4e-37;
 Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDWKPSBDPMDQNAKCY 60
 DB 265 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDWKPSBDPMDQNAKCY 324
 QY 61 PGCKYTL 66
 DB 325 PGCKYTL 330
 RESULT 21
 AAW19745

ID AAW19745 standard; protein; 496 AA.
 XX
 AC AAW19745;
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Mouse inhibitor of apoptosis protein homologue MHA.
 XX
 KM Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHA;
 KW degenerative disease; infectious disease; autoimmune disease; cancer;
 XX therapy; diagnosis.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 26..93
 FT /label= BIR
 FT Region 163..230
 FT /label= BIR
 FT Region 264..330
 FT /label= BIR
 FT Region 448..485
 FT /label= RING_finger
 XX
 PN WO9723501-A1.
 XX
 PD 03-JUL-1997.
 XX
 PF 20-DEC-1996; 96MO-AU000827.
 XX
 XX 22-DEC-1995; 95AU-00007275.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Vaux DL;
 XX
 XX WPI; 1997-350966/32.
 DR N-PSDB; AAT72710.
 XX
 PT Isolated protein homologues of viral inhibitors of apoptosis - used to
 PT modulate apoptosis for treatment of degenerative, infectious or
 PT auto-immune diseases and cancer.
 XX
 PS Claim 7; Page 44-47; 136pp; English.
 XX
 CC Mammalian IAP homologue A (MHA) (AAW19745) is a murine homologue of
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence
 CC was deduced from a cDNA clone (see also AAT72710) isolated from a mouse
 CC liver cDNA library on the basis of homology to Oryza pseudotsugata
 CC polyhedrosis virus IAP BIR and RING finger amino acid motifs (see also
 CC AAW19744). IAP homologues (see also AAW19746-52) and their derivatives
 CC and chemical analogues can be used in methods for modulating apoptosis in
 CC animal cells, specifically for treatment, by inhibition, of degenerative
 CC and infectious disease or, by promotion, of cancer and autoimmune disease
 CC
 XX
 SQ Sequence 496 AA;
 XX
 Query Match 92.5%; Score 357; DB 2; Length 496;
 Best Local Similarity 93.9%; Pred. No. 8.6e-36;
 Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDWKPSBDPMDQNAKCY 60
 DB 264 YEARIYFGTWIYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDWKPSBDPMDQNAKCY 323
 QY 61 PGCKYTL 66
 DB 324 PGCKYTL 329
 RESULT 22
 ADB61820
 ID ADB61820 standard; protein; 66 AA.

ADBE1820;
04-DEC-2003 (first entry)
Human inhibitor of apoptosis (IAP) protein testis IAP BIR2 domain.
baculovirus inhibitor of apoptosis repeat domain; BIR domain;
apoptosis pathway; embryonic development; viral pathogenesis; cancer;
autoimmune disorder; neurodegenerative disease; apoptotic response;
systemic lupus erythematosus; multiple sclerosis; viral infection;
herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
HIAP1, CIAP2, HIAP2, CIAP1, RING zinc finger; caspase-3; caspase-7;
caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
cervical cancer; uterine cancer; testicular cancer;
small cell lung carcinoma; uterine cancer; renal cell carcinoma;
Wilm's tumour; human, BIR 2 domain.
Homo sapiens.
MO2003040172-A2.
15-MAY-2003.
12-NOV-2002; 2002MO-CA001738.
09-NOV-2001; 2001US-0332300P.
08-APR-2002; 2002US-0370934P.
(AEGE-) AEGERA THERAPEUTICS INC.
Boudreault A, Korneluk RG, La Casse E, Liston P;
WPI; 2003-513532/48.
Polypeptide capable of forming a complex with a polypeptide comprising a
baculovirus inhibitor of apoptosis repeat domain useful for treating
cancer and other neoplasms.
Disclosure; Fig 1A; 53pp; English.
This invention relates to a substantially pure polypeptide having a
length of less than 100 amino acids and capable of forming a complex with
a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
(BIR) domain. The apoptosis pathway is known to play a critical role in
embryonic development, viral pathogenesis, cancer, autoimmune disorders
and neurodegenerative diseases. The failure of the apoptotic response has
been implicated in the development of cancer, autoimmune disorders (for
example systemic lupus erythematosus and multiple sclerosis) and viral
infections (including herpes virus, poxvirus and adenovirus). The
inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
(CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
-9 which are proteases involved in the initiation of apoptosis. Compounds
which inhibit the activity of IAPs may therefore have cytostatic activity
through the enhancement of apoptosis. The polypeptides of the invention
are candidate peptide ligands for binding to the BIR domain of IAPs. They
may be useful for the treatment of cancer and other neoplasms, such as
leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
and Wilm's tumour, and for enhancing apoptosis. The present sequence is
that of the human inhibitor of apoptosis (IAP) protein testis IAP BIR2
domain which was used to demonstrate homology to other human IAP protein
BIR domains to which the peptides of the invention are targeted to bind.
Sequence 66 AA;
Query Match 86.5%; Score 334; DB 7; Length 66;
Best Local Similarity 81.8%; Pred. No. 6.3e-34;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0

DB 1 YEARLITFTGTMWYVYNKEQLARAGFYALIGQEDKVCFCFHGGGLANKPKEDPWEQNAKMY 60

OY 61 PGCKYL 66
|||||

Db 61 PGCKYL 66

RESULT 23
AA81440
ID AA81440 standard; protein; 236 AA.
XX
AC AA81440;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human TIAP (an inhibitor of apoptosis).
XX
KW TIAP; inhibitor of apoptosis protein; IAP; X-linked IAP; XIAP;
KW internal ribosome entry site; IRES; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00121979.
PR 14-JUN-1999; 99US-0032319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
XX
DR WPI: 2000-338644/29.
DR N-PSDB; AAN06940.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
XX site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 82; 87pp; English.
XX

The invention relates to the identification of modulators of cap-independent translation and apoptosis. The method comprises exposing a test compound to an X-linked inhibitor of apoptosis protein (XIAP) internal ribosome entry site (IRES) reporter cistron, and determining the amount of translation from the XIAP IRES reporter cistron exposed to the compound relative to the translation from the unexposed XIAP IRES reporter cistron. A relative increase in translation from the exposed XIAP IRES reporter cistron indicates a compound that increases XIAP IRES-dependent (cap independent) translation. XIAP protein plays a critical role in the regulation of apoptosis by suppressing activation of downstream caspase-3 and caspase-7. Compounds identified by the method which decrease XIAP IRES-dependent translation (thus leading to reduced expression of XIAP and hence increasing apoptosis) can be used for treating cancer. The methods can also be used for the identification of agents that upregulate XIAP translation and hence inhibit apoptosis, which can be used to treat autoimmune diseases, degenerative diseases or immunorejection. Such agents may, for example, be used to inhibit apoptosis of neurons in conditions such as Alzheimer's disease; islet cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial infarction. They can also be used to enhance the survival of cell or organ transplants. XIAP IRES elements can also be incorporated into expression constructs which encode XIAP or other IAPs (inhibitor of apoptosis proteins, e.g., TIAP; AA81440). Such constructs may be used in gene therapy to inhibit apoptosis in a cell. The present sequence represents human TIAP (an inhibitor of apoptosis protein), DNA encoding which may be used in an expression vector comprising a XIAP IRES element

```

XX  Sequence 236 AA;
SQ
Query Match      86.5%; Score 334; DB 3; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY  1 YEARIYTFGTWYISVKNKQLARAGFYALGEGDVKYCFHCGGGLTDMKPSDDPMDQNAKCY 60
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  4 YEARIITFGTMYISVKNKQLARAGFYALGEGDVKYCFHCGGGLANMKPKEDPWEQNAKMY 63
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  61 PGCKYKL 66
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  64 PGCKYKL 69
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 24
AAE00365
ID  AAE00365 standard; protein; 236 AA.
XX
AC  AAE00365;
XX
DT  19-JUN-2001 (first entry)
XX
DE  Human IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
XX
KW  Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW  chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
KW  TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW  cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KW  T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KW  retinal degeneration; hyperferitinaemia-cataract syndrome; cancer;
KW  autoimmune disease; diabetes; multiple sclerosis; cyrostatic.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Domain 7..70
    /label= BIR domain
    /note= "Baculovirus iap repeat"
    /label= .223
    /label= RING_finger_domain
XX
PN  WO200123568-A2.
XX
PD  05-APR-2001.
XX
PF  29-SEP-2000; 2000WO-US026735.
XX
PR  30-SEP-1999; 99US-0157169P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Duckett C, Mir SS;
XX
DR  WPI: 2001-258135/26.
XX
DR  N-PSDB; AAD03581.
XX
PT  Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT  transforming growth factor beta receptor modulating activity, and the
PT  nucleic acids that encode them, useful for treating, e.g. diabetes and
PT  multiple sclerosis.
XX
PS  Claim 1; Fig 2; 108pp; English.
XX
XX  The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC  (ILP-2). The ILP-2 gene is located on chromosome 19q13.3-q13.4. ILP-2
CC  comprises a single amino-terminal domain known as baculovirus iap repeat
CC  (BIR), followed by a spacer region and a carboxy-terminal ring finger
CC  domain. It interacts with transforming growth factor beta receptor
CC  (TGFbetaR) and modulates TGFbetaR activity. It also potentially inhibits
CC  apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It
CC  also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in

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CC  the area of genetic testing for predisposition to diseases, such as cone-
CC  rod retinal dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell
CC  acute lymphoblastic leukaemia, colorectal cancer and hyperferitinaemia-
CC  cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also
CC  used in the treatment of diseases associated with abnormal apoptosis such
CC  as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
CC  neurodegenerative diseases including retinal degeneration. The ILP-2 gene
CC  is also used in gene therapy for treating patients suffering from ILP-2
CC  gene deletions or mutations
XX
SQ  Sequence 236 AA;
Query Match      86.5%; Score 334; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY  1 YEARIYTFGTWYISVKNKQLARAGFYALGEGDVKYCFHCGGGLTDMKPSDDPMDQNAKCY 60
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  4 YEARIITFGTMYISVKNKQLARAGFYALGEGDVKYCFHCGGGLANMKPKEDPWEQNAKMY 63
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  61 PGCKYKL 66
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  64 PGCKYKL 69
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 25
AAU75066
ID  AAU75066 standard; protein; 236 AA.
XX
AC  AAU75066;
XX
DT  23-APR-2002 (first entry)
XX
DE  Human testes specific inhibitor of apoptosis (TIAP) protein.
XX
KW  TIAP; apoptosis; testes specific inhibitor of apoptosis; human;
KW  apoptotic; cyrostatic; anti-infertility; contraceptive;
KW  chromosome 12q22-23; transgenic animal; antibody; immunogen;
KW  testicular cell; testicular cancer; cancer; male infertility;
KW  male birth control; XIAP.
XX
OS  Homo sapiens.
XX
PN  US6331412-B1.
XX
PD  18-DEC-2001.
XX
PF  29-JAN-1999; 99US-00239867.
XX
PR  29-JAN-1998; 98US-0073001P.
XX
PA  (UYOT-) UNIV OTTAWA.
XX
PI  Korneluk RG, Lagace M;
XX
DR  WPI: 2002-105275/14.
XX
DR  N-PSDB; ABK3197.
XX
PT  Nucleic acids encoding a testis specific apoptosis inhibitor protein
PT  (TIAP) useful for treating testicular cancers, cancers in non-testicular
PT  tissues, male infertility, and for achieving male birth control.
XX
PS  Example 4; Fig 4B; 29pp; English.
XX
XX  This invention relates to a novel isolated nucleic acid molecule encoding
CC  a TIAP polypeptide (testes-specific inhibitor of apoptosis) protein. This
CC  gene is a homologue of the X-linked XIAP gene and is located on
CC  chromosome 12q22-23. The nucleotide and protein sequences of the
CC  invention, and vectors containing these sequences may be used in the
CC  prevention, treatment and diagnosis of diseases associated with
CC  inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC  be used to express the TIAP protein by recombinant methods. Conversely,
CC  antisense nucleic acid molecules may be administered to down-regulate

```

CC TIAP expression. The nucleotide sequence, may also be used to design DNA
CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
CC detect and quantitate the presence of similar nucleic acid sequences in
CC samples, to identify patients who may be in need of restorative therapy.
CC Through the production of transgenic animals and cells, the sequences may
CC also be used to study the expression and function of TIAP proteins and
CC their role in metabolism. The TIAP polypeptides may be used to produce
CC antibodies against TIAP and maybe used to identify modulators (agonists
CC and antagonists) of TIAP expression and activity. An anti-TIAP antibody
CC or antagonist may also be used to down-regulate TIAP expression and
CC activity. The reagents may be used in this way for the treatment of
CC excessive or insufficient apoptosis, particularly in testicular cells. In
CC particular they are useful in diagnosing and treating testicular cancers,
CC cancers in non-testicular tissues, male infertility, and for achieving
CC male birth control. The present sequence represents the human TIAP
CC protein sequence of the invention
XX
SQ Sequence 236 AA;

Query Match 86.5%; Score 334; DB 5; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIYTFGWIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDDPMQHAKEY 60
DB 4 YEARLITFGTWMYSVNKEQLARAGFYALGQEDKVQCFHCGGGLANMKPKEDPMQHAKEY 63
QY 61 PGCKYTL 66
DB 64 PGCKYTL 69

RESULT 26
ABG32417 standard; protein; 236 AA.
ID ABG32417
AC ABG32417;

DT 15-NOV-2002 (first entry)

DE Inhibitor of apoptosis protein, TIAP.

XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
KM fertility; testicular cancer; male infertility; male birth control.
XX Mammalia.

OS
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by nm; start codon is illegible in
FT specification"

PN US2002086409-A1.

PD 04-JUL-2002.

PF 18-DEC-2001; 2001US-00024433.

PR 29-JAN-1998; 98US-0073001P.

PR 29-JAN-1999; 99US-00239867.

PA (KORN/) KORNELUK R G.

PA (LAGA/) LAGACE M.

PI Korneluk RG, Lagace M;

DR WPI: 2002-642245/69.

DR N-PSDB; ABSS2802.

XX Novel polypeptide, a member of inhibitor of apoptosis family of proteins
PT that is expressed in testes useful for modulating apoptosis in cells,
PT particular cells involved in male fertility.
XX

PS Example 3; Fig 4B; 24pp; English.

XX A substantially pure TIAP polypeptide (1), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (1) is
CC useful for identifying a compound that modulates TIAP biological activity
CC (1) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (1) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. TIAP may be manipulated for use as a male
CC birth control. TIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the amino
CC acid sequence of TIAP
XX

SQ Sequence 236 AA;

Query Match 86.5%; Score 334; DB 5; Length 236;
Best Local Similarity 81.8%; Pred. No. 2.8e-33;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIYTFGWIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDDPMQHAKEY 60
DB 4 YEARLITFGTWMYSVNKEQLARAGFYALGQEDKVQCFHCGGGLANMKPKEDPMQHAKEY 63
QY 61 PGCKYTL 66
DB 64 PGCKYTL 69

RESULT 27
AAU75747 standard; protein; 464 AA.
ID AAU75747
AC AAU75747;

DT 08-MAY-2002 (first entry)

DE Human Inhibitor of apoptosis protein 7 (IAPL7) protein.

XX Human; inhibitor of apoptosis 7; IAPL7; cytosolic; antiapoptotic; IAP;
KM apoptosis; V-Rel; cancer; NF-kappaB; chromosome 19; vaccine;
XX gene therapy; hyperproliferative disease; transgenic animal; antibody.
XX Homo sapiens.

OS
FH Key Location/Qualifiers
FT Region 1..133
FT /note= "This sequence is specifically claimed in claim 1
FT of the specification and is encoded by the nucleic acid
FT represented in ABK14678"

PN WO200210381-A1.

PD 07-FEB-2002.

PF 18-JUL-2001; 2001WO-EP008287.

PR 28-JUL-2000; 2000EP-00116452.

PA (MERE) MERCK PATENT GMBH.

PI Hentsch B;

DR WPI: 2002-188741/24.

DR P-PSDB; ABK14677.

XX New inhibitor of apoptosis proteins and polynucleotides useful in
PT vaccines for inducing an immune response against hyperproliferative
PT diseases e.g. cancer.
XX
XX Claim 1; Page 35-36; 41pp; English.

PS This invention relates to the nucleic acid and protein sequences of a
XX

XX Gorilla IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
 XX
 XX
 KM Gorilla; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
 KM transforming growth factor beta receptor; TGFbetaR; cytosolic;
 KM c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
 KM cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
 KM T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 KM retinal degeneration; hyperferritinemia-cataxact syndrome; cancer;
 KM autoimmune disease; diabetes; multiple sclerosis.
 XX
 OS Gorilla gorilla.
 XX
 PN W0200123568-A2.
 XX
 PD 05-APR-2001.
 XX
 PD 29-SEP-2000; 2000WO-US026735.
 XX
 PR 30-SEP-1999; 99US-0157169P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Duckert C, Mir SS;
 XX
 DR WPI; 2001-258135/26.
 DR N-PSDB; AAD03583.
 XX
 PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
 PT transforming growth factor beta receptor modulating activity, and the
 PT nucleic acids that encode them, useful for treating, e.g. diabetes and
 PT multiple sclerosis.
 XX
 PS Claim 1; Fig 2; 108bp; English.
 XX
 XX The present sequence is gorilla inhibitor of apoptosis (IAP)-like protein
 CC -2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain known as
 CC baculovirus iap repeat (BIR), followed by a spacer region and a carboxy-
 CC terminal ring finger domain. It interacts with transforming growth factor
 CC beta receptor (TGFbetaR) and modulates TGFbetaR activity. It also
 CC potentially inhibits apoptosis induced by overexpression of Bax or by
 CC Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
 CC activity. ILP-2 is used in the area of genetic testing for predisposition
 CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
 CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
 CC and hyperferritinemia-cataxact syndrome owing to an ILP-2 deletion or
 CC mutation. The ILP is also used in the treatment of diseases associated
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
 CC diabetes and multiple sclerosis and neurodegenerative diseases including
 CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
 CC treating patients suffering from ILP-2 gene deletions or mutations
 CC
 XX Sequence 236 AA;
 SQ
 Query Match 84.2%; Score 325; DB 4; Length 236;
 Best Local Similarity 79.8%; Pred. No. 3.7e-32;
 Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEARIITFGTWIYVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPDQAKCY 60
 DB 4 YEALITFGTWIYVYNKEQLARAGFYALGSDGVKCFHCGGGLANMKPKEDPMQHAQMY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69
 RESULT 32
 ADB61832
 ID ADB61832 standard; protein. 57 AA.
 AC ADB61832;
 XX

DT 04-DEC-2003 (first entry)
 XX
 XX Unidentified inhibitor of apoptosis (IAP) protein IAP BIR3 domain.
 XX
 KM baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KM autoimmune disorder; neurodegenerative disease; apoptotic response;
 KM systemic lupus erythematosus; multiple sclerosis; viral infection;
 KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KM XIAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KM caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KM cervical cancer; uterine cancer; testicular cancer;
 KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KM Wilms' tumor; BIR 3 domain.
 XX
 OS Unidentified.
 XX
 PN W02003040172-A2.
 XX
 PD 15-MAY-2003.
 XX
 PD 12-NOV-2002; 2002WO-CA001738.
 XX
 PR 09-NOV-2001; 2001US-0332300P.
 PR 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Boudreault A, Korneluk RG, La Casse E, Liston P;
 XX
 DR WPI; 2003-513532/48.
 XX
 PT Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating a
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1B; 53bp; English.
 XX
 XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example, systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus. The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAPI
 CC (CIAP2) and HIAPI1 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumor, and for enhancing apoptosis. The present sequence is
 CC that of an unidentified inhibitor of apoptosis (IAP) protein IAP BIR3
 CC domain which was used to demonstrate homology to human IAP protein BIR
 CC domains to which the peptides of the invention are targeted to bind.
 XX
 SQ Sequence 57 AA;
 Query Match 79.3%; Score 306; DB 7; Length 57;
 Best Local Similarity 91.1%; Pred. No. 1.7e-30;
 Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 11 WIVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPDQAKCYPGCKYL 66
 DB 2 WIVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPDQAKHMGCKYL 57

RESULT 33
AD139821
ID AD139821 standard; protein; 53 AA.
AC AD139821;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NAIP BIRa region #1.
XX
XX Inhibitor of apoptosis-like protein; iap; i1p; apoptosis; therapy;
XX cancer; cell immortalisation; cysteine protease; viral infection;
XX cytoskeletal; vincristine; baculovirus iap-like repeat; BIR; human;
XX neutral apoptosis inhibitory protein; NAIP.
XX
XX Homo sapiens.
XX
XX US6511828-B1.
XX
XX 28-JAN-2003.
XX
XX 31-MAY-1996; 96US-00657759.
XX
XX 31-MAY-1996; 96US-00657759.
XX
XX 31-MAY-1996; 96US-00657759.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Thompson CB, Duckett CS;
XX
XX WPI; 2003-391256/37.
XX
XX
XX New inhibitor of apoptosis-like protein (i1p) and polynucleotide encoding
XX i1p, useful for inhibiting or stimulating apoptosis in target cells,
XX treating certain cancers, or sustaining host cell survival following
XX viral infection.
XX
XX Example 2; SEQ ID NO 19; 42pp; English.
XX
XX The present invention relates to inhibitor of apoptosis (iap)-like
XX proteins (i1p) and polynucleotides encoding such proteins. Sequences of
XX the invention are useful for inhibiting or stimulating apoptosis in
XX target cells or for treating certain cancers. They are also useful in the
XX immortalisation of cells for culture, for inhibiting the activation of
XX cysteine proteases and to sustain host cell survival following viral
XX infection. The i1p may also be used as a marker in gel separation
XX procedures or as a standard in protein concentration determinations. The
XX present sequence is human neutral apoptosis inhibitory protein (NAIP).
XX baculovirus iap-like repeat (BIR) region.
XX
XX
XX Sequence 53 AA;
SQ
Query Match 72.3%; Score 279; DB 7; Length 53;
Best Local Similarity 95.9%; Pred. No. 3.9e-27;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 18 EQIARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKCYPGCKYL 66
DB 1 EQIARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKWYPGCKYL 49
RESULT 34
ADB61829
ID ADB61829 standard; protein; 66 AA.
AC ADB61829;
XX
XX 04-DEC-2003 (first entry)
XX
XX Chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
XX Baculovirus inhibitor of apoptosis repeat domain; BIR domain;
XX apoptosis pathway; embryonic development; viral pathogenesis; cancer;
XX

KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilms' tumour; BIR 3 domain; chicken.
XX
XX Gallus gallus.
XX
XX WO2003040172-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-CA001738.
XX
XX 09-NOV-2001; 2001US-0332300P.
XX
XX 08-APR-2002; 2002US-0370934P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Boudreaux A, Korneluk RG, La Casse E, Lipton P;
XX
XX WPI; 2003-513532/48.
XX
XX
XX Polypeptide capable of forming a complex with a polypeptide comprising a
XX baculovirus inhibitor of apoptosis repeat domain useful for treating
XX cancer and other neoplasms.
XX
XX Disclosure; Fig 1B; 53pp; English.
XX
XX This invention relates to a substantially pure polypeptide having a
XX length of less than 100 amino acids and capable of forming a complex with
XX a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
XX (BIR) domain. The apoptosis pathway is known to play a critical role in
XX embryonic development, viral pathogenesis, cancer, autoimmune disorders
XX and neurodegenerative diseases. The failure of the apoptotic response has
XX been implicated in the development of cancer, autoimmune disorders (for
XX example systemic lupus erythematosus and multiple sclerosis) and viral
XX infections (including herpes virus, poxvirus and adenovirus. The
XX inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
XX more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
XX (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
XX terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
XX -9 which are proteases involved in the initiation of apoptosis. Compounds
XX which inhibit the activity of IAPs may therefore have cytostatic activity
XX through the enhancement of apoptosis. The polypeptides of the invention
XX are candidate peptide ligands for binding to the BIR domain of IAPs. They
XX may be useful for the treatment of cancer and other neoplasms, such as
XX leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
XX cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
XX and Wilms' tumour, and for enhancing apoptosis. The present sequence is
XX that of the chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
XX which was used to demonstrate homology to human IAP protein BIR domains
XX to which the peptides of the invention are targeted to bind.
XX
XX
XX Sequence 66 AA;
SQ
Query Match 72.3%; Score 279; DB 7; Length 66;
Best Local Similarity 71.2%; Pred. No. 4.9e-27;
Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 1 YEARIYTFGTWIVSVNKEQIARAGFYALGSDGVKCFHCGGGLTDMKPSDDPMDQAKCY 60
DB 1 YERRIOTFLAWIYVPVKKHLEAGFYSTGNBHVVCYFHCGGGLQEMKENEDPMDQAKWF 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66
RESULT 35

ADK34975
 ID ADK34975 standard; protein; 151 AA.
 XX
 AC ADK34975;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Novel human polypeptide SeqID7057.
 XX
 KM antiarthritic; antiparkinsonian; neuroprotective; nootropic;
 KM immunosuppressive; cytostatic; antipsoriatic; antiinflammatory;
 KM antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
 KM arthritic; Parkinson's; Alzheimer's; autoimmune disease; cancer;
 KM psoriasis; inflammatory bowel disease; infection; bacteria; virus;
 KM fungus; parasite; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..151
 FT /label= OTHER
 FT /note= "OTHER= All Xaa's in this sequence are unknown
 amino acids or the site of a stop codon within the DNA
 sequence"
 FT
 FT
 XX
 XX
 XX
 PD 28-FEB-2002.
 XX
 PF 05-MAR-2001; 2001MO-US004941.
 XX
 PR 07-MAR-2000; 2000US-00519705.
 PR 19-MAY-2000; 2000US-00574454.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2002-280918/32.
 XX
 PT Isolated polynucleotide encoding bone marrow derived polypeptides useful
 for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
 PT disease, and inflammatory bowel disease.
 PT
 XX
 PS Claim 20; SEQ ID NO 7057; 504pp; English.
 XX
 CC This invention relates to a novel isolated polynucleotide comprising a
 CC nucleotide sequence selected from one of 1680 sequences, a mature protein
 CC coding portion of them, an active domain of them and their complementary
 CC sequences. The invention may be useful for the production of compounds
 CC with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
 CC immunosuppressive, cytostatic, antipsoriatic, antiinflammatory,
 CC antibacterial, antiviral, antifungal or antiparasitic activity. In
 CC addition, the disclosed sequences may be useful for gene therapy. The
 CC polypeptides or their antibodies are useful for treating many diseases
 CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
 CC psoriasis, inflammatory bowel disease and infections caused by bacteria,
 CC viruses, fungi or parasites. The present sequence is that of a human
 CC polypeptide of the invention.
 CC
 XX
 SQ Sequence 151 AA;
 Query Match 67.4%; Score 260; DB 5; Length 151;
 Best Local Similarity 71.2%; Pred. No. 3.1e-24;
 Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 QY 1 YEARIIVFTGWIYSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMDOHAKCY 60
 DB 6 YEAGIITLGMWYVSVNQAHGAFYALGKGDYKVCFCGGRRLTDMKPIEHPROGHAKWY 65
 QY 61 PGCKYL 66
 DB 66 PRCKYL 71

RESULT 36
 ADB61830
 ID ADB61830 standard; protein; 52 AA.
 XX
 AC ADB61830;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Bovine inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
 XX
 KM baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KM apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KM autoimmune disorder; neurodegenerative disease; apoptotic response;
 KM systemic lupus erythematosus; multiple sclerosis; viral infection;
 KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KM H1AP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KM caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
 KM cervical cancer; uterine cancer; testicular cancer;
 KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KM Wilms tumour; BIR 3 domain; bovine; cow.
 XX
 OS Bos taurus.
 XX
 XX
 PN WO2003040172-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 12-NOV-2002; 2002MO-CA001738.
 XX
 PR 09-NOV-2001; 2001US-0332300P.
 PR 08-APR-2002; 2002US-0370934P.
 XX
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Boudreault A, Korneluk RG, La Casse E, Liston P;
 XX
 DR WPI; 2003-513532/48.
 XX
 PT Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 PT
 XX
 PS Disclosure; Fig 1B; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms tumour, and for enhancing apoptosis. The present sequence is
 CC that of the bovine inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC to which the peptides of the invention are targeted to bind.
 CC
 XX
 SQ Sequence 52 AA;

CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HIRAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms tumor, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein HAPI BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

XX Sequence 68 AA;

Query Match 51.3%; Score 198; DB 7; Length 68;
 Best Local Similarity 55.9%; Pred. No. 7.2e-17;
 Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFGTWIVS--VNKEQLARAGFYALGEGDKVXCFCFGGGLTDMKSEDPMDQHA 58
 Db 1 HAAAFKTFFWMPSSVLVNPEQLASAGFYVGNSDVXCFCCDGLRCWESGDDPMVQHA 60
 QY 59 CYPGCKYL 66
 Db 61 WPRCEYL 68

RESULT 39

ADO26592 standard; protein; 442 AA.

AC ADO26592;

DT 01-JUL-2004 (first entry)

XX Human APl2.

XX Chromosome translocation; malignancy;
 KW mucosa-associated lymphoid tissue-lymphoma associated translocation;
 KM MALT; MALT; primary cell transformation; apoptosis inhibitor 2; APl2;
 KM tumour; cytostatic; human.

OS Homo sapiens.

XX US6689875-B1.

PN 10-FEB-2004.

PF 26-MAY-2000; 2000US-00579692.

PR 09-JUN-1999; 99US-0138834P.

PA (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Dierlamm J, Beens M, Marlijnen P;

XX WPI; 2004-141430/14.

DR N-PSDB; ADO26591.

PT New mucosa-associated lymphoid tissue-lymphoma associated translocation
 protein, useful in diagnosing and treating tumors.

XX Disclosure; SEQ ID NO 58; 88bp; English.

XX The present invention relates to a method for characterisation of
 CC chromosome translocation T (11;18) (q21;q21) and its association with
 CC malignancies such as mucosa-associated lymphoid tissue (MALT)-lymphomas.
 CC Also disclosed are: the polynucleotide and polypeptide sequences for
 CC human mucosa-associated lymphoid tissue (MALT)-lymphoma associated
 CC translocation (MALT), and a novel mechanism of primary cell transformation

CC by expression of a fusion protein comprising at least apoptosis inhibitor
 CC 2 (APl2) fused to another protein such as MALT. The MALT polynucleotide and
 CC polypeptide sequences, and the method of the invention are useful in
 CC diagnosing and treating tumors. The present sequence represents human
 CC APl2.

XX Sequence 442 AA;

Query Match 51.3%; Score 198; DB 8; Length 442;
 Best Local Similarity 55.9%; Pred. No. 6.4e-16;
 Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFGTWIVS--VNKEQLARAGFYALGEGDKVXCFCFGGGLTDMKSEDPMDQHA 58
 Db 255 HAAAFKTFFWMPSSVLVNPEQLASAGFYVGNSDVXCFCCDGLRCWESGDDPMVQHA 314

QY 59 CYPGCKYL 66
 Db 315 WPRCEYL 322

RESULT 40

ABP72159 standard; protein; 557 AA.

AC ABP72159;

DT 22-APR-2003 (first entry)

XX Inhibitor of apoptosis protein CIAP2.

XX Inhibitor of apoptosis; CIAP2; apoptosis; cancer; leukemia; lymphoma;

KW neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX Unidentified.

XX WO2003004606-A2.

PN 16-JAN-2003.

PF 03-JUL-2002; 2002WO-US021002.

XX 03-JUL-2001; 2001US-00898158.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

DR N-PSDB; ABZ58104.

PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 17A; 124pp; English.

XX The present sequence is the protein sequence of inhibitor of apoptosis
 CC protein CIAP2. The invention provides a nucleic acid, such as an
 CC antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MAPI, MAPI2,
 CC MAPI3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukemia, acute myelogenous
 CC leukemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 557 AA;

Query Match 51.3%; Score 198; DB 6; Length 557;
 Best Local Similarity 55.9%; Pred. No. 8.4e-16;

Matches	38;	Conservative	6;	Mismatches	22;	Indels	2;	Gaps	1;
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Db	255	HAAFPKTFFFMPPSSVLVNPEQLASAGFYVYGNSDVDKCFCCDGLRCWESGDDPWOQAK	314						
Qy	59	CYPCKYL	66						
Db	315	WPPRCXYL	322						

Search completed: June 15, 2005, 17:35:44
 Job time : 117 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:39:48 ; Search time 108.5 Seconds

(without alignments)
233.180 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
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Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	386	100.0	66 9 US-09-201-936-24	Sequence 24, Appl
2	386	100.0	66 16 US-10-600-272-24	Sequence 24, Appl
3	386	100.0	496 9 US-09-974-592-10	Sequence 10, Appl
4	386	100.0	496 9 US-09-201-936-10	Sequence 10, Appl
5	386	100.0	496 16 US-10-636-065-225	Sequence 225, App
6	386	100.0	496 16 US-10-600-272-10	Sequence 10, Appl
7	372	96.4	496 16 US-10-482-952-5	Sequence 5, Appl
8	366	94.8	66 9 US-09-201-936-25	Sequence 25, Appl
9	366	94.8	66 16 US-10-600-272-25	Sequence 25, Appl
10	366	94.8	107 9 US-09-965-967-20	Sequence 20, Appl
11	366	94.8	236 13 US-10-024-433-4	Sequence 4, Appl

12	366	94.8	278 9 US-09-964-899-39	Sequence 39, Appl
13	366	94.8	497 9 US-09-974-592-4	Sequence 4, Appl
14	366	94.8	497 9 US-09-201-936-4	Sequence 4, Appl
15	366	94.8	497 15 US-10-366-307-2	Sequence 2, Appl
16	366	94.8	497 16 US-10-636-065-219	Sequence 219, App
17	366	94.8	497 16 US-10-600-272-4	Sequence 4, Appl
18	334	86.5	236 13 US-10-024-433-2	Sequence 2, Appl
19	334	86.5	464 15 US-10-343-115-2	Sequence 2, Appl
20	233	60.4	50 14 US-10-138-618-28	Sequence 28, Appl
21	233	60.4	50 14 US-10-138-618-29	Sequence 29, Appl
22	233	60.4	50 14 US-10-138-618-32	Sequence 32, Appl
23	198	51.3	68 16 US-09-201-936-26	Sequence 26, Appl
24	198	51.3	68 16 US-10-600-272-26	Sequence 26, Appl
25	198	51.3	557 16 US-10-482-952-9	Sequence 9, Appl
26	198	51.3	604 9 US-09-974-592-6	Sequence 6, Appl
27	198	51.3	604 9 US-09-201-936-6	Sequence 6, Appl
28	198	51.3	604 14 US-10-232-286-4	Sequence 4, Appl
29	198	51.3	604 14 US-10-141-618-6	Sequence 6, Appl
30	198	51.3	604 15 US-10-366-307-6	Sequence 6, Appl
31	198	51.3	604 16 US-10-636-065-221	Sequence 221, App
32	198	51.3	604 16 US-10-600-272-6	Sequence 6, Appl
33	198	51.3	604 16 US-10-730-476A-79	Sequence 79, Appl
34	198	51.3	604 16 US-10-825-282-40	Sequence 40, Appl
35	198	51.3	604 17 US-10-934-717-4	Sequence 4, Appl
36	198	51.3	1140 14 US-10-353-461-8	Sequence 8, Appl
37	190	49.2	68 9 US-09-201-936-28	Sequence 28, Appl
38	190	49.2	68 14 US-10-041-859-18	Sequence 18, Appl
39	190	49.2	68 16 US-10-600-272-28	Sequence 28, Appl
40	190	49.2	172 14 US-10-041-859-12	Sequence 12, Appl
41	190	49.2	268 14 US-10-323-643-10	Sequence 10, Appl
42	189	49.0	600 9 US-09-974-592-12	Sequence 12, Appl
43	189	49.0	600 16 US-10-482-952-1	Sequence 1, Appl
44	185	47.9	68 14 US-10-041-859-14	Sequence 14, Appl
45	185	47.9	172 14 US-10-041-859-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-201-936-24
Query Match 100.0%; Score 386; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 66; Conservative 0; Mismatches 0; Gaps 0;

QY	1	YEAIIVFGWITVSVNKEQLARAGFYALGEGDKVCFHCGGSLTDWKPSDSDPMDQAKCY	60
Dd	1	YEAIIVFGWITVSVNKEQLARAGFYALGEGDKVCFHCGGSLTDWKPSDSDPMDQAKCY	
QY	61	PGCKYL	66
Dd	61	PGCKYL	66

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RESULT 2
US-10-600-272-24
: Sequence 24, Application US/10600272
: Publication No. US20040157232A1
: GENERAL INFORMATION:
: APPLICANT: Korneljuk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/00306
: CURRENT APPLICATION NUMBER: US/10/600,272
: CURRENT FILING DATE: 2003-06-20
: PRIOR APPLICATION NUMBER: US 09/011,356
: PRIOR FILING DATE: 1998-02-04
: PRIOR APPLICATION NUMBER: PCT/IB96/01022
: PRIOR FILING DATE: 1996-08-05
: PRIOR APPLICATION NUMBER: US 08/576,956
: PRIOR FILING DATE: 1995-12-22
: PRIOR APPLICATION NUMBER: US 08/511,485
: PRIOR FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 66
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-600-272-24

Query Match      100.0%; Score 386; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps

QY      1 YEARIVTFGWITSVYNKEQLARAGFALGSGDKYKCGCGGLTDPKPSBDPMDQAKCY 60
DB      1 YEARIVTFGWITSVYNKEQLARAGFALGSGDKYKCGCGGLTDPKPSBDPMDQAKCY 60

QY      61 PGCKYL 66
DB      61 PGCKYL 66

RESULT 3
US-09-974-592-10
: Sequence 10, Application US/09974592
: Patent No. US20020120121A1
: GENERAL INFORMATION:
: APPLICANT: Korneljuk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009004
: CURRENT APPLICATION NUMBER: US/09/974,592
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 08/800,929
: PRIOR FILING DATE: 1997-02-13

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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: prt
; ORGANISM: Mus musculus
US-09-974-592-10

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RESULT 4
US-09-201-936-10
; Sequence 10, Application US/09201936
; Publication No. US20020187946X1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Lifson, Peter
; TITLE OF INVENTION: NANOMALIAN TAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: SeqSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

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RESULT 5
US-10-636-065-225
; Sequence 225, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Kornelius, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin

APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 225
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-10-636-065-225

Query Match 100.0%; Score 386; DB 16; Length 496;
Best Local Similarity 100.0%; Pred. No. 1e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 264 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 6
US-10-600-272-10
Sequence 10, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003006
CURRENT APPLICATION NUMBER: US/10/600,272
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: PCT/IB96/01022
PRIOR FILING DATE: 1996-08-05
PRIOR APPLICATION NUMBER: US 08/576,956
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: US 08/511,485
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-10-600-272-10

Query Match 100.0%; Score 386; DB 16; Length 496;
Best Local Similarity 100.0%; Pred. No. 1e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 264 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 7

US-10-482-952-5
Sequence 5, Application US/10482952
Publication No. US20040254136A1
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University in the City of New York, et al.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CELL
FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
CURRENT APPLICATION NUMBER: US/10/482,952
CURRENT FILING DATE: 2004-01-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 496
TYPE: PRT
ORGANISM: human
US-10-482-952-5

Query Match 96.4%; Score 372; DB 16; Length 496;
Best Local Similarity 97.0%; Pred. No. 5.3e-37;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
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QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 8
US-09-201-936-25
Sequence 25, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: PCT/IB96/01022
PRIOR FILING DATE: 1996-08-05
PRIOR APPLICATION NUMBER: US 08/576,956
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: US 08/511,485
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 9; Length 66;
Best Local Similarity 95.5%; Pred. No. 3.4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 1 YEARIYFTGWTIVSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDPMDOHAKCY 60

QY 61 PGCKYL 66
DB 61 PGCKYL 66

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RESULT 9
US-10-600-272-25
; Sequence 25, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-25
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Query Match          94.8%; Score 366; DB 16; Length 66;
Best Local Similarity 95.5%; Pred. No. 3,4e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKMY 60
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Qy 61 PGCKYL 66
Db 61 PGCKYL 66
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RESULT 10
US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: FU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20
```

```
Query Match          94.8%; Score 366; DB 9; Length 107;
Best Local Similarity 95.5%; Pred. No. 5,7e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKCY 60
Db 15 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKMY 74
```

```
Qy 61 PGCKYL 66
Db 75 PGCKYL 80
```

```
RESULT 11
US-10-024-433-4
; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-4
```

```
Query Match          94.8%; Score 366; DB 13; Length 236;
Best Local Similarity 95.5%; Pred. No. 1,3e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKCY 60
Db 4 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKMY 63
```

```
Qy 61 PGCKYL 66
Db 64 PGCKYL 69
```

```
RESULT 12
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39
```

```
Query Match          94.8%; Score 366; DB 9; Length 278;
Best Local Similarity 95.5%; Pred. No. 1,6e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKCY 60
Db 46 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDPMDOHAKMY 105
```

```
Qy 61 PGCKYL 66
Db 106 PGCKYL 111
```

RESULT 13
US-09-974-592-4
Sequence 4, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Prate, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 14
US-09-201-936-4
Sequence 4, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 15
US-10-366-307-2
Sequence 2, Application US/10366307
Publication No. US20030224399A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: Method for Determining the Prognosis
TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
FILE REFERENCE: P-LJ 5659
CURRENT APPLICATION NUMBER: US/10/366,307
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 60/356,956
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-10-366-307-2

Query Match 94.8%; Score 366; DB 15; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGSDVKVCFHCGGGLTDMKPSRSDPMDQAKMY 324
Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 16
US-10-636-065-219
Sequence 219, Application US/10636065
Publication No. US20040127694A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Theracof
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 219
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-10-636-065-219

```
Query Match          94.8%; Score 366; DB 16; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKMY 324

Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 17
US-10-600-272-4
; Sequence 4, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-4

Query Match          94.8%; Score 366; DB 16; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 265 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKMY 324

Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 18
US-10-024-433-2
; Sequence 2, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-2

Query Match          86.5%; Score 334; DB 13; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.1e-32;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 4 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKMY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 19
US-10-343-115-2
; Sequence 2, Application US/10343115
; Publication No. US20040072999A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: Novel inhibitor of apoptosis protein
; FILE REFERENCE: IAPL-7BHW
; CURRENT APPLICATION NUMBER: US/10/343,115
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-115-2

Query Match          86.5%; Score 334; DB 15; Length 464;
Best Local Similarity 81.8%; Pred. No. 2.3e-32;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKCY 60
Db 232 YEARIVTFTGWTIVSVNKEQLARAGFYALGEGDKVCKCFHCGGGLTDMKPSDPMDOHAKMY 291

Qy 61 PGCKYL 66
Db 292 PGCKYL 297

RESULT 20
US-10-138-618-28
; Sequence 28, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 5.7e-21;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 40

RESULT 21
US-10-138-618-29
Sequence 29, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 5.7e-21;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 40

RESULT 22
US-10-138-618-32
Sequence 32, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match 60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 5.7e-21;
Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDMKPSDPMDOHAKYPGCKYL 40

RESULT 23
US-09-201-936-26
Sequence 26, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; PRIOR FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; PRIOR FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26
```

```

Query Match      51.3%; Score 198; DB 9; Length 68;
Best Local Similarity 55.9%; Pred. No. 1.6e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
```

```

QY 1 YEARIVTFGTWYS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
Db 1 HAARFKTFPMWPSVVLNPEQLASAGFYVGNSDVYKFCDCDGLRCWESGDDPMVQHAH 60
```

```

QY 59 CYPGCKYL 66
Db 61 WPPRCETL 68
```

```

RESULT 24
US-10-600-272-26
; Sequence 26, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; EARLIER APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-26
```

```

Query Match      51.3%; Score 198; DB 16; Length 68;
Best Local Similarity 55.9%; Pred. No. 1.6e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
```

```

QY 1 YEARIVTFGTWYS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
```

```

Db 1 HAARFKTFPMWPSVVLNPEQLASAGFYVGNSDVYKFCDCDGLRCWESGDDPMVQHAH 60
QY 59 CYPGCKYL 66
Db 61 WPPRCETL 68
```

```

RESULT 25
US-10-482-952-9
; Sequence 9, Application US/10482952
; Publication No. US20040254136A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York, et al.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CELL
; FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
; CURRENT APPLICATION NUMBER: US/10/482,952
; PRIOR FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 557
; TYPE: PRT
; ORGANISM: human
US-10-482-952-9
```

```

Query Match      51.3%; Score 198; DB 16; Length 557;
Best Local Similarity 55.9%; Pred. No. 1.5e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
```

```

QY 1 YEARIVTFGTWYS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
Db 255 HAARFKTFPMWPSVVLNPEQLASAGFYVGNSDVYKFCDCDGLRCWESGDDPMVQHAH 314
```

```

QY 59 CYPGCKYL 66
Db 315 WPPRCETL 322
```

```

RESULT 26
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; APPLICANT: Baird, Robert G.
; APPLICANT: Teang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6
```

```

Query Match      51.3%; Score 198; DB 9; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;
```

```

QY 1 YEARIVTFGTWYS--VNKEQLARAGFYALGEGDKVCKFCGGLTDMKRSDDPMQHAH 58
```


Db	Qy	Db
255 HAARFKFFFWPSSVYNPEQLASAGFYTVGNSDDVKCFCDGGLRCHESGSDPEWVQHAH	59 CYPCKKYL 66	314
	: :	
	315 WPPRCETL 322	

```

RESULT 27
US-09-201-936-6
/ Sequence 6, Application US/09201936
/ Publication No. US20020187946A1
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Mackenzie, Alexander E.
/ APPLICANT: Baird, Stephen
/ APPLICANT: Liéton, Peter
/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
/ TITLE OF INVENTION: PROBES, AND DETECTION METHODS
/ FILE REFERENCE: 07891/003003
/ CURRENT APPLICATION NUMBER: US/09/201,936
/ EARLIER FILING DATE: 1998-12-01
/ EARLIER APPLICATION NUMBER: 09/011,356
/ EARLIER FILING DATE: 1998-02-04
/ EARLIER APPLICATION NUMBER: PCT/IB96/01022
/ EARLIER FILING DATE: 1996-08-05
/ EARLIER APPLICATION NUMBER: 08/576,956
/ EARLIER FILING DATE: 1995-12-22
/ EARLIER APPLICATION NUMBER: 08/511,485
/ EARLIER FILING DATE: 1995-08-04
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 604
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ US-09-201-936-6

```

Query Match	51.3%	Score 198	DB 9	length 604
Best Local	Similarly	35.9%	Pred. No. 1.7e-15	
Matches 38	Conservative	6	Mismatches 22	Indels 2
				Gaps 1

Qy 1 YEARI VTFCGIWIS--VNKEQLARACGYALGEGDKVCKFHCGGGGLTDWKPSDEPDQAK 58
 : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 255 HAARFKTFENWPSSVLNPEGLASAFYYGVGSDDYKCFCCGGGLRCHESGDDPFWYGHAK 314

Db 315 WFPRC EYL 322

RESULT 28
 US-10-232-286-4
 ; Sequence 4, Application US/10232286
 ; Publication No. US20030143579A1
 GENERAL INFORMATION:
 APPLICANT: Roche, Mike
 Goedel, David V
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLHRH, HOHBACH, TEST, ALBERTSON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 City: San Francisco
 State: California
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/232,286

```

1      FILING DATE: 30-AUG-2002
2      CLASSIFICATION: <Unknown>
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US/08/569,749
5      FILING DATE: <Unknown>
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Brezner, David J.
8      REGISTRATION NUMBER: 24, 774
9      REFERENCE/DOCKET NUMBER: A-62464/DJB
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: (415)781-1989
12     TELEFAX: (415)398-3249
13     INFORMATION FOR SEQ ID NO: 4:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 604 amino acids
16     TYPE: amino acid
17     STRANDEDNESS: single
18     TOPOLOGY: linear
19     MOLECULE TYPE: protein
20     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
21     US-10-232-286-4

```

SEQUENCE DESCRIPTION:	SEQ ID NO:
US-10-232-286-4	4:

Query Match	51.3%	Score 198;	DB 14;	Length 604;
Best Local Similarity	55.9%	Pred. No. 1.7e-15;		
Matches 38; Conservative	6;	Mismatches 22;	Indels 2;	Gaps 1

[illegible]

```
QY      59 CYPGCKYL 66
          :||:|
Db     315 WFPRCXYL 322
```

```

RESULT 29
US-10-141-618-6
; Sequence 6, Application US/10141618
; Publication No. US20030165867A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methode For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-1J 5254
; CURRENT APPLICATION NUMBER: US/10/141, 618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeqq For Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-141-618-6

```

Query Match	51.3%;	Score 198;	DB 14;	Length 604;
Best Local Similarity	55.9%;	Pred. No. 1.7e-15;		
Matches 38;	Conservative 6;	Mismatches 22;	Indels 2;	Gaps 1;

DQ 1 YKRIIVTGTWIS--VNKEQLARAGFYALGEGDKYCFHCGGGGLTDWKPSSEDPMDQAK 58
:
255 HAARFKTEFNWPSSVLVNPBQLASAGFYFYGNSSDVKCFCCDDGLCWESESDDPMTQIAK 314

```
QY      59 CYPGCKYL  66
      :|:|:|
Db     315 WPPRCEYL 322
```

RESULT 30
US-10-366-307-6
; Sequence 6, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; TITLE OF INVENTION: For Patients with a Prostate Neoplastic Condition
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366.307
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-307-6

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVVLVNPBQLASAGFYVGNSDVVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 31
US-10-636-065-221
; Sequence 221, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636.065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-636-065-221

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVVLVNPBQLASAGFYVGNSDVVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 32

US-10-600-272-6
; Sequence 6, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600.272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-6

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVVLVNPBQLASAGFYVGNSDVVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322

RESULT 33
US-10-730-476A-79
; Sequence 79, Application US/10730476A
; Publication No. US20040171105A1
; GENERAL INFORMATION:
; APPLICANT: Du, Chunying
; APPLICANT: Yang, Qiheng
; TITLE OF INVENTION: Method and Composition for Cleaving IAPs
; FILE REFERENCE: 40716(IP-022)
; CURRENT APPLICATION NUMBER: US/10/730.476A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 79
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-730-476A-79

Query Match 51.3%; Score 198; DB 16; Length 604;
Best Local Similarity 55.9%; Pred. No. 1.7e-15;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYTFGTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMDQHA 58
DB 255 HAARFTFFWMPSSVVLVNPBQLASAGFYVGNSDVVKCFCCDGLRCMESGDDPMDQHA 314

QY 59 CYPGCKYL 66
DB 315 WFPRCETL 322


```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
; US-09-201-936-28

```

```

Query Match          49.2%; Score 190; DB 9; Length 68;
Best Local Similarity 48.5%; Pred. No. 1,6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

```

```

QY 3 ARIVTGTWIVSYVK--EQLARAGFYALGEGDKVCFHCGGGLTWKPSSEDPMDQHAKCY 60
DB 3 ARIRTFAEWPRGLKQRPBELAENGFFYTGQSDKTRCFCCDGLKDWEPDAPMGOHARWY 62

```

```

QY 61 PGCKYL 66
DB 63 DRCEYV 68

```

```

RESULT 38
US-10-041-859-18
; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
; US-10-041-859-18

```

```

Query Match          49.2%; Score 190; DB 14; Length 68;
Best Local Similarity 48.5%; Pred. No. 1,6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

```

```

QY 3 ARIVTGTWIVSYVK--EQLARAGFYALGEGDKVCFHCGGGLTWKPSSEDPMDQHAKCY 60
DB 3 ARIRTFAEWPRGLKQRPBELAENGFFYTGQSDKTRCFCCDGLKDWEPDAPMGOHARWY 62
QY 61 PGCKYL 66
DB 63 DRCEYV 68

```

```

RESULT 39
US-10-600-272-28
; Sequence 28, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
; US-10-600-272-28

```

```

Query Match          49.2%; Score 190; DB 16; Length 68;
Best Local Similarity 48.5%; Pred. No. 1,6e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

```

```

QY 3 ARIVTGTWIVSYVK--EQLARAGFYALGEGDKVCFHCGGGLTWKPSSEDPMDQHAKCY 60
DB 3 ARIRTFAEWPRGLKQRPBELAENGFFYTGQSDKTRCFCCDGLKDWEPDAPMGOHARWY 62

```

```

QY 61 PGCKYL 66
DB 63 DRCEYV 68

```

```

RESULT 40
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
; US-10-041-859-12

```

```

Query Match          49.2%; Score 190; DB 14; Length 172;
Best Local Similarity 48.5%; Pred. No. 4,2e-15;
Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

```

```

QY 3 ARIVTGTWIVSYVK--EQLARAGFYALGEGDKVCFHCGGGLTWKPSSEDPMDQHAKCY 60

```

Db	70	ARLRTFAEWPRGLKQRPBELAEGFFYTGQGDKTRCFCDCDGLKDWEPPDAPM	QOHARWY 129
Qy	61	PGCKYL	66
Db	130	DRCEYV	135

Search completed: June 15, 2005, 17:58:16
Job time : 110.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2005, 17:27:02 ; Search time 23.5 Seconds
(without alignments)
270.226 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYTFGTWIVSVNKEQL.....KPSDPWDQHAQCYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	94.8	497	2	S69544 apoptotic inhibitor
2	198	51.3	604	2	S68449 apoptotic inhibitor
3	196	50.8	358	2	UCS964 apoptotic inhibitor
4	190	49.2	268	2	T10304 inhibitor of apopt
5	190	49.2	268	2	A53989 apoptosis-inhibi
6	184	47.7	618	2	S68450 apoptosis inhibito
7	177	45.9	298	2	UC7568 kidney inhibitor o
8	175	45.3	275	2	A45679 inhibitor-of-apopt
9	164.5	42.6	1232	2	A55478 neuronal apoptosis
10	160.5	41.6	1447	2	T42628 apoptosis inhibito
11	149	38.6	496	2	S68452 apoptosis inhibito
12	149	38.6	497	2	S69545 apoptosis inhibito
13	141	36.5	208	2	T03183 probable apoptosis
14	128	33.2	275	2	T10310 apoptosis-inhibiti
15	126	32.6	150	2	T28409 ORF MSV248 probabl
16	114.5	29.7	4845	2	T31067 BIR repeat contain
17	108	28.0	286	2	D36828 orf13 protein - Au
18	106	27.5	292	2	T41772 IAP1 orf27 - Bomby
19	100	25.9	155	2	T37471 apoptosis inhibito
20	99	25.6	155	2	T30489 apoptosis inhibito
21	93	24.1	308	2	T37474 apoptosis inhibito
22	84.5	21.9	997	2	T43523 cut17 protein - fi
23	83.5	21.6	329	2	T28403 ORF MSV242 probabl
24	80.5	20.9	564	2	C42523 A55R protein - vac
25	80.5	20.9	564	2	J01792 Salp17R protein -
26	66.5	17.2	187	2	T50621 hypotheoretical prote
27	66	17.1	511	2	T33634 hypotheoretical prote
28	66	17.1	534	2	T25720 hypotheoretical prote
29	65.5	17.0	737	2	P00219 RNA-2 polypeptide

30	65	16.8	466	2	PC4296 nicotinic acetylch
31	64.5	16.7	334	2	S39502 vegetative storage
32	64.5	16.7	506	2	S13720 coat protein - ara
33	64	16.6	204	2	H70609 probable dna-3-met
34	63	16.3	249	2	H72858 apoptosis inhibito
35	62.5	16.2	336	2	H81785 conserved hypothe
36	61.5	15.9	336	2	B81210 conserved hypothe
37	61.5	15.9	1808	2	T15099 hypotheoretical prote
38	60.5	15.7	437	2	AG0766 probable dehydrata
39	60.5	15.7	788	2	S70079 1,4-alpha-glucan b
40	60.5	15.7	1798	2	S53869 laminin beta-2 cha
41	60	15.5	246	2	I50127 MHC class II histo
42	60	15.5	249	2	T41814 IAP2 orf17 - Bomby
43	60	15.5	252	2	I50126 MHC class II histo
44	59.5	15.4	459	2	S76138 hypotheoretical prote
45	59.5	15.4	607	2	T39823 hypotheoretical prote

ALIGNMENTS

```

RESULT 1
S69544
apoptosis inhibitor IAP homolog - human
C:/Species: Homo sapiens (man)
C:/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:/Accession: S69544; S68451
R:/Duckett, C.S.; Nava, V.B.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillefilian, M.C
EMBO J. 15, 2685-2694, 1996
A:/Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:/Reference number: S69544; MUID:96256286; PMID:8654366
A:/Accession: S69544
A:/Status: preliminary; nucleic acid sequence not shown
A:/Molecule type: mRNA
A:/Residues: 1-497 <DUC>
A:/Cross-References: UNIPROT:P98170; EMBL:U32974; NID:G1016687; PID:ACS0518.1; PID:G101
R:/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:/Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:/Reference number: A58182; MUID:96149249; PMID:8552191
A:/Accession: S68451
A:/Status: nucleic acid sequence not shown
A:/Molecule type: mRNA
A:/Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:/Cross-References: EMBL:U45880; NID:G1184319; PID:AA050373.1; PID:G1184320
C:/Genetics:
A:/Gene: ilp
C:/Function:
A:/Description: apoptotic suppressor
C:/Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:/Keywords: Apoptosis; zinc finger
F:/446-490/Domain: RING finger homology <RRN>

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 2e-33;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEARIYTFGTWIVSVNKEQLAPAGFYALGSGDKVCKFCGCGGLTDMKPSDPWDQHAQCY 60
DB 265 YEARIYTFGTWIVSVNKEQLAPAGFYALGSGDKVCKFCGCGGLTDMKPSDPWDQHAQCY 324

OY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 2
S68449
apoptosis inhibitor iap-1 - human
C:/Species: Homo sapiens (man)
C:/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:/Accession: S68449
R:/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,

```


RESULT 5

RESULT 11
S68452
apoptosis inhibitor diap - fruit fly (*Drosophila melanogaster*)

[illegible]

```

Db      167 FHRRLATPQNFIRIDKRNRYKCTSKLAKAGMFISANKKDTSAKCPCLVEL-DPDESD 225
QY      52 PWDQAKCTYPGCKYL 66
      ||::||::
Db      226 PWEEHQKFSASCDPI 240

RESULT 22
T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43523; T41649; T41700
R:Morishita, J.; Matsunaka, T.; Yanagida, M.
submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cut17 is required for chromosome segregation.
A:Reference number: Z22536
A:Accession: T43523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <MOR>
A:Cross-references: UNIPROT:Q14064; EMBL:AB031034; PIDN:BAAB3415.1
R:Harries, D.; Wood, V.; Rajandream, M.A.; Barrall, B.G.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z22007
A:Accession: T41649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <HAR>
A:Cross-references: EMBL:AL031323; PIDN:CA20434.1; GSPDB:GN00068; SPDB:SPCC962.02C
R:Experimental source: strain 972h-; cosmid c962
R:Medler, H.; Dueserhoef, A.; McDougall, R.C.; Rajandream, M.A.; Barrall, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z22010
A:Accession: T41700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 932-997 <MED>
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10C
C:Genetics:
A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c
A:Map position: 3L
A:Introns: 43/3

Query Match      21.9%; Score 84.5; DB 2; Length 997;
Best Local Similarity 30.3%; Pred. No. 0.17;
Matches 23; Conservative 8; Mismatches 34; Indels 11; Gaps 3;

QY      1 YEARIYVTEGTWYISYVK--EQIARAGFY--ALGEG-----DKYKCFHGGGLTDPKPS 49
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db      22 YSKRIIDTFQKKKMPAPKPPETLATVGFYNPISSENSBERLDNVTCYMCCKSFYDWEED 81
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
QY      50 EDPWDQAKCTYPGCKY 65
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db      82 DDPLEKHITHSPSCPW 97
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::

RESULT 23
T28403
OMP MSV242 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomop
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28403
R:Afonso, C.L.; Tullman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:95102612; PMID:9847359
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-329 <APO>
A:Cross-references: UNIPROT:Q91YK0; EMBL:AF063866; NID:g4049647; PIDN:AAC97721.1; PID:g4049647; C:Genetics:

```


RESULT 28
T25720
hypothetical protein F21F3.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25720
R:Geisels, C.; Kramer, J.; Elliott, G.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid F21F3.
A:Reference number: Z20075
A:Accession: T25720
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-534 <GRI>
A:Cross-references: EMBL:U88175; PIDN:AAB42282.1; GSPDB:GN00019; CESP:F21F3.5
A:Experimental source: strain Bristol N2; clone F21F3
C:Genetics:
A:Gene: CESP:F21F3.5
A:Map position: 1
A:Introns: 43/2; 66/3; 118/2; 168/3; 248/3; 271/3; 364/1; 507/3
A:Superfamily: acetylcholine receptor

	Query Match	17.1%	Score 66;	DB 2;	Length 534;	
	Best Local Similarity	27.6%	Pred. No. 11;			
	Matches	21;	Conservative	9;	Mismatches	20; Indels 26; Gaps 4
QY	8 FGTWLYSYN-----KEQLARAGFYALBEGDKYKCFHGGGLTDMKPSDPMWD	54				
	: : : : : : : : :					
Db	169 FGSMFSSNNLSVELNEPSSLRYEEIIDEKGII---DNVTVAEDGIDISDYPSVE-WD	222				
QY	55 -----DHAKCYPGC	63				
	:					
Db	223 IMSRVAKRRATNYPCSC	238				

RESULT 29
P00219
RNA-2 polypotein - arabis mosaic virus (fragment)
N/Contains: coat protein
C/Species: arabis mosaic virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: P00219; P00220
J/Bertolotti, D. J.; Harris, R. D.; Edwards, M. L.; Cooper, J. I.; Hawes, W. S.
J. Gen. Virol. 72, 1801-1809, 1991
A/Title: Transgenic plants and insect cells expressing the coat protein of arabis mosaic virus
A/Reference number: P00219; MUID:91341466; PMID:1875193
A/Accession: P00219
A/Molecule type: genomic RNA
A/Residues: 1-737 <BBR>
A/Cross-references: UNIPROT:O65028; GB:DI10086; NID:G221017; PIDN:BAA00982.1; PID:dl00145
A/Experimental source: strain 11ac
A/Accession: P00220
A/Molecule type: Protein
A/Residues: 233-252 <BE2>
C/Genetics:
A/Map position: segment RNA-2
C/Keywords: polypotein
C/233-737/Product: coat protein #status experimental <COA>

Query Match	17.0%	Score 65.5;	DB 2;	Length 737;
Best Local Similarity	32.3%	Pred. No. 17;		
Matches 20; Conservative	8;	Mismatches 19;	Indels 15;	Gaps 4;

Qy 12 IYSVNEQLARAGFYALGEGDKYK-----CFHCGGGL-----TDMKPSDEPDMDHAKCYP 61
 Db 447 VYNNNNNTLLS-----YYLGIGGVAKGKHICSPCTTGYGLVRVVSSEMGVNTNNMQLK-YIP 501
 Qy 62 GC 63
 Db 502 GC 503

RESULT 30
 PC4236
 nicotinic acetylcholine receptor alpha chain - nematode (*Trichostrongylus colubriformis*)
 N:Alternate names: tar-1 protein
 C:Species: *Trichostrongylus colubriformis*
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C:Accession: PC4236
 R:Wiley, L.J.; Weiss, A.S.; Sangster, N.C.; Li, Q.
 Gene 182, 97-100, 1996
 A:Title: Cloning and sequence analysis of the candidate nicotinic acetylcholine receptor
 A:Reference number: PC4236; MUID:97136696; PMID:892073
 A:Accession: PC4236
 A:Molecule type: DNA
 A:Residues: 1-466 <MTL>
 A:Cross-references: UNIPROT:Q94789; GB:U56903
 C:Genetics:
 A:Gene: tar-1
 C:Superfamily: acetylcholine receptor
 F:214-239/Domain: transmembrane #status predicted <TM1>
 F:247-270/Domain: transmembrane #status predicted <TM2>
 F:276-299/Domain: transmembrane #status predicted <TM3>
 F:415-436/Domain: transmembrane #status predicted <TM4>

```

Query Match      16.8%  Score 65; DB 2; Length 466;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 20; Conservative 11; Mismatches 19; Indels 26; Gaps 4.

QY      8  FGTWITYSYN-----KEQLARAGFYALAGEBGRKVCFCFGGGLTMMKPSDEPDWD 54
Db       126 FGSWTYSNNLNLLELLENNARYEEELINESGVV-----DNITLADGIDLSDYPSVSE-WD 179

QY      55  -----QHAKCYPGC 63
Db       180 IMSRVARRRSKINYPSC 195

```

```

RESULT 31
S39502
vegetative storage protein win4.5 - western balsam poplar x cottonwood (fragment)
C:Species: Populus trichocarpa x Populus deltoides (western balsam poplar x cottonwood)
C:Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S39502
R:David, J.M.; Egelnköt, E.E.; Coleman, G.D.; Chen, T.H.H.; Haiszig, B.E.; Riemenschneit
Plant Mol. Biol. 23, 135-143, 1993
A:Title: A family of wound-induced genes in Populus shares common features with genes enc
A:Reference number: S39502; MUID:94033285; PMID:8106009
A:Accession: S39502
A:Molecule type: mRNA
A:Residues: 1-324 <DNA>
A:Cross-references: UNIPROT:O41097; EMBL:L20233; NID:G309838; PID:G309839

Query Match      16.7%   Score 64.5   DB 2   Length 324;
Best Local Similarity 32.8%   Pred. No. 10;
Matches 22; Conservative 4; Mismatches 24; Indels 17; Gaps 3;

```

[illegible]

```

RESULT 32
S13720
coat protein - arabis mosaic virus (fragment)
C/Species: arabis mosaic virus
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S137200 S77995
R:/Seiikelner, H.; Himmeler, G.; Matzanovich, D.; Kattinger, H.
Nucleic Acids Res. 18, 7182, 1990

```

A/Title: Nucleotide sequence of AMV-capsid protein-gene.
A/Reference number: S13720; MUID:91088343; PMID:2263501
A/Accession: S13720
A/Molecule type: genomic RNA
A/Residues: 1-506 <STE>
A/Cross-references: UNIPROT:P24819; EMBL:X55460
A/Accession: S77995
A/Molecule type: protein
A/Residues: 2-21 <HM>
A/Keywords: polypeptide
P:2-506/Product: coat protein #status predicted <COA>

Query Match 16.7%; Score 64.5; DB 2; Length 506;
Best Local Similarity 32.3%; Pred. No. 16;
Matches 20; Conservative 8; Mismatches 19; Indels 15; Gaps 4;

Qy 12 IYSNKEQLARAGFYALGEGDKVCK-----CFHCGGL-----TWKPSSEDPWDQAKCYG 61
Db 216 VYNNFTLLS-----YVIGIGIVGKRVKVCSPCTGYIVLRVSBMNGVTNNMQLFK-Y 270

Qy 62 GC 63
Db 271 GC 272

RESULT 33
H70609
probable dna-3-methyladenine glycosylase I - Mycobacterium tuberculosis (strain H37Rv)

C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: H70609

R/Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: H70609

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-204 <COL>

A/Cross-references: UNIPROT:O05311; GB:Z93777; GB:AL123456; NID:G3261726; PIDN:CAB07833

A/Experimental source: strain H37Rv

C/Genetics:

A/Gene: tagA

C/Superfamily: 3-methyladenine DNA glycosylase I

Query Match 16.6%; Score 64; DB 2; Length 204;
Best Local Similarity 31.8%; Pred. No. 7.5;
Matches 21; Conservative 7; Mismatches 22; Indels 16; Gaps 3;

Qy 9 GTWYISVKNK-----QLARAGFYALGEGDKVCKCFHCGGLTD-----WKPSEDPWDQAK 57
Db 139 GSELPSTSTSKAMSRKRGFRFVGPTTAYALMQRATGMVDHIOACWPTFRPFDQ-- 196

Qy 58 KCVPGC 63
Db 197 ---PGC 199

RESULT 34
H72858
apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus

C/Species: Autographa californica nuclear polyhedrosis virus, AcMNPV

A/Note: dsDNA virus

C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C/Accession: H72858

R/Araya, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A/Reference number: A72850; MUID:94303173; PMID:8030224

A/Accession: H72858

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <AYR>
A/Cross-references: UNIPROT:P41454; GB:J22858; NID:G510708; PIDN:AAA66701.1; PID:G559140
A/Genes: Ac-IAP2

Query Match 16.3%; Score 63; DB 2; Length 249;
Best Local Similarity 32.1%; Pred. No. 12;
Matches 17; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

Qy 14 SVNKEQLARAGFYALGEGDKVCKCFHCGGLTDWKPSEDPWDQAKCYGCKYL 66
Db 103 SVVVDMLARGFYFYGKAGHRCSCG-HVFKYKSYDDAQRHKKQ--NCKFL 151

RESULT 35
H81785

conserved hypothetical protein NMA2139 [imported] - Neisseria meningitidis (strain Z2491

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: H81785

R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]

; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: H81785

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-336 <PAR>

A/Cross-references: UNIPROT:Q9JST8; GB:AL162758; GB:AL157959; NID:G7380672; PIDN:CAB85353

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA2139

C/Superfamily: Haemophilus influenzae conserved hypothetical protein HI0634

Query Match 16.2%; Score 62.5; DB 2; Length 336;
Best Local Similarity 30.6%; Pred. No. 18;
Matches 19; Conservative 7; Mismatches 17; Indels 19; Gaps 3;

Qy 1 YEARIYFTGWIYSVKNKEQLARAGFYALGEGDKVCKCFHCG-----GGLTWKPSSEDP 52
Db 28 YMARQTRNTWLYS-----EMVNAQAIYVGDKDFLMEEGEPVALQLG-----SDP 76

Qy 53 WD 54
Db 77 SD 78

RESULT 36
B81210

conserved hypothetical protein NMB0348 [imported] - Neisseria meningitidis (strain MC58

C/Species: Neisseria meningitidis

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: B81210

R/Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

Li, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignault, V.; Pizze, M.

Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A/Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: B81210

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-336 <TEB>

A/Cross-references: UNIPROT:Q9K142; GB:AE002391; GB:AE002098; NID:G7225561; PIDN:AAE40793

A/Experimental source: serogroup B, strain MC58

C/Genetics:

A/Gene: NMB0348

C/Superfamily: Haemophilus influenzae conserved hypothetical protein HI0634

```
Query Match 15.9%; Score 61.5; DB 2; Length 336;
Best Local Similarity 30.6%; Pred. No. 23;
Matches 19; Conservative 7; Mismatches 17; Indels 19; Gaps 3;

OY 1 YEARIYVETWIVYVKNKQLARAGFYALGSGDKYKCHCG-----GGITDMPKPEDP 52
DB 28 YIARQITRNTWLVIS-----EMVNAQAIYVGDQKDFLMTFNEGQPVALQLQGG-----SDP 76

OY 53 WD 54
DB 77 SD 78

RESULT 37
T15099
hypochemical protein W03P8.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15099
R/Johnson, D.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03P8.
A/Reference number: Z18293
A/Accession: T15099
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1808 <OH>
A/Cross-references: UNIPROT:Q44565; EMBL:AF039041; NID:g2736380; PID:g2736386; PIDN:AA59
A/Experimental source: strain Bristol N2; clone W03P8
C/Genetics:
A/Map position: 4
A/Intons: 99/2; 255/2; 365/2; 435/3; 565/2; 975/2; 1055/2; 1602/3; 1719/3; 1766/1
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
F/797-842/Domain: laminin-type EGF-like homology <LEG>

Query Match 15.9%; Score 61.5; DB 2; Length 1808;
Best Local Similarity 40.9%; Pred. No. 1.2e+02;
Matches 9; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

OY 32 DKVCFHCGGGLTDMKPSDDPW 53
DB 74 EQTKCFYC-DSRTMKPQRPXPY 94

RESULT 38
AG0766
probable dehydratase RfBH rfBH [imported] - Salmonella enterica subsp. enterica serovar
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0766
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Crohin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moutle, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AG0766
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-437 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD02453.1; PID:G16503320; GSPDB:GN00176
C/Genetics:
A/Gene: rfBH
C/Superfamily: erythromycin resistance protein

Query Match 15.7%; Score 60.5; DB 2; Length 437;
Best Local Similarity 31.9%; Pred. No. 39;
Matches 22; Conservative 4; Mismatches 26; Indels 17; Gaps 4;

OY 1 YEARIYVETWIVYVKNKQLARAGFY-----ALGSGDKYKCHCGGGLTDMKPSDDPW 54
```

```
DB 200 YEARMVGTFC-----DIGTSFYPAHHTMGGAIV-FTKSGELKTIIESPRDWG 248
OY 55 QHAKCYPGC 63
DB 249 RDCYCAPGC 257

RESULT 39
S70079
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I - Streptomyces coelicolor
N/Alternate names: glycogen branching enzyme
C/Species: Streptomyces coelicolor
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S70079; T42040
R/Brunon, C.U.; Plaskitt, K.A.; Chater, K.F.
Mol. Microbiol. 18, 89-99, 1995
A/Title: tissue-specific glycogen branching isoenzymes in a multicellular prokaryote, St
A/Reference number: S70078; MUID:96154943; PMID:8596463
A/Accession: S70079
A/Molecule type: DNA
A/Residues: 1-788 <BRU>
A/Cross-references: UNIPROT:Q59833; EMBL:X83397; NID:g1061285; PIDN:CA58314.1; PID:g1061
A/Experimental source: strain A3(2)
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
A/Note: only a part of the nucleic acid sequence is shown
C/Genetics:
A/Gene: glgBI
A/Start codon: GNG
C/Superfamily: 1,4-alpha-glucan branching enzyme
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 15.7%; Score 60.5; DB 2; Length 788;
Best Local Similarity 35.6%; Pred. No. 68;
Matches 21; Conservative 3; Mismatches 18; Indels 17; Gaps 4;

OY 9 GTWIVYVKNKQLARAGFYA-----LGGDKYK-----CFHCG-GGLTDMKPSDDPWQHA 57
DB 348 GSWGYGV-----TSFYAPYARLGDPPDFKTLVDRHRAIGLVLMDWVPAHFPRDWA 399

RESULT 40
S53869
laminin beta-2 chain precursor (version 2) - human
N/Alternate names: s-laminin
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C/Accession: S53869
R/Itivannan, A.; Vuoleenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggv
Matric Biol. 14, 489-497, 1994
A/Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss
A/Reference number: S53869
A/Accession: S53869
A/Molecule type: mRNA
A/Residues: 1-1798 <ITV>
A/Cross-references: UNIPROT:P55268
C/Genetics:
A/Gene: GDB:LAMB2
A/Cross-references: GDB:132363; OMIM:150325
A/Map position: 3p21.3-3p21.2
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C/Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F/1-32/Domain: signal sequence #status predicted <SIG>
F/33-1798/Product: laminin beta-2 chain #status predicted <MAT>
F/283-344/Domain: laminin-type EGF-like homology <LEB1>
F/347-407/Domain: laminin-type EGF-like homology <LEB2>
F/410-467/Domain: laminin-type EGF-like homology <LEB3>
F/470-519/Domain: laminin-type EGF-like homology <LEB4>
F/522-552/Domain: laminin-type EGF-like homology #status atypical <LEB5>
F/783-828/Domain: laminin-type EGF-like homology <LEB6>
F/831-874/Domain: laminin-type EGF-like homology <LEB7>
F/877-924/Domain: laminin-type EGF-like homology <LEB8>
```


F,927-983/Domain: laminin-type EGF-like homology <LE09>
 F,986-1035/Domain: laminin-type EGF-like homology <LE10>
 F,1038-1092/Domain: laminin-type EGF-like homology <LE11>
 F,1095-1140/Domain: laminin-type EGF-like homology <LE12>
 F,1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 15.7%; Score 60.5; DB 2; Length 1798;
 Best local Similarity 32.7%; Pred. No. 1.5e+02;
 Matches 16; Conservative 5; Mismatches 25; Indels 3; Gaps 2;

OY 19 QLARAGFYALGEGDKVKCFHCGGGLTDWKPSSEDPWDQHA-KCYPGCKYL 66
 Db 450 QQCRDGFPGGLISDRLGCRRCQCNARGTVPGSTPCDPNPGSGCY--CKRL 496

Search completed: June 15, 2005, 17:40:28
 Job time : 25.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 15, 2005, 17:19:12 ; Search time 112.5 Seconds
(without alignments)
300.420 Million cell updates/sec

Title: US-10-600-272-24

Perfect score: 386
Sequence: 1 YEARIYFTGWTIYSVNKEQL.....KPSEDPWDQAKCYPGCKYL 66

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	94.8	496	1 BIR4 RAT	Q9R016 rat1us norv
2	366	94.8	496	2 Q9ESF0	Q9ESF0 rat1us norv
3	366	94.8	497	1 BIR4 HUMAN	P98170 homo sapien
4	366	94.8	501	2 Q9EQ04	Q9EQ04 rat1us norv
5	361	93.5	501	2 Q9EQ05	Q9EQ05 rat1us norv
6	357	92.5	496	1 BIR4 MOUSE	Q60989 mus musculu
7	334	86.5	236	1 BIR8 HUMAN	Q60989 mus musculu
8	334	86.5	236	2 Q6PIY1	Q6PIY1 homo sapien
9	328	85.0	236	1 BIR8 PANTR	Q9SM72 pan troglod
10	325	84.2	236	1 BIR8 GORGO	Q9SM71 gorilla gor
11	306	79.3	106	2 Q9ERW6	Q9ERW6 homo sapien
12	279	72.3	493	2 Q9UVR8	Q9UVR8 gallus galli
13	258	66.8	109	2 Q8WMT4	Q8WMT4 bos taurus
14	258	66.8	109	2 Q8DBV7	Q8DBV7 brachydantio
15	212	54.9	322	2 Q8UW12	Q8UW12 brachydantio
16	212	54.9	405	2 Q8UW12	Q8UW12 brachydantio
17	212	54.9	415	2 Q7SXU1	Q7SXU1 brachydantio
18	204	52.8	280	2 Q6TV93	Q6TV93 chorisstenu
19	198	51.3	604	1 BIR3 HUMAN	Q13489 homo sapien
20	196	50.8	287	2 Q6E7G7	Q6E7G7 antiscaris
21	196	50.8	358	1 P1AP PIG	Q65640 sus scrofa
22	192	49.7	195	2 Q9IA70	Q9IA70 gallus galli
23	192	49.7	197	2 Q9IA69	Q9IA69 gallus galli
24	192	49.7	602	2 Q9ESB9	Q9ESB9 rat1us norv
25	192	49.7	611	1 BIR CHICK	Q90660 gallus galli
26	190	49.2	268	1 IAP3 NPVOP	P41437 oryzae peen
27	189	49.0	269	2 Q6OX56	Q6OX56 agrotis seg
28	189	49.0	374	2 Q921N0	Q921N0 mus musculu
29	189	49.0	600	1 BIR3 MOUSE	Q08863 mus musculu
30	189	49.0	616	2 Q804E2	Q804E2 ictalurus p
31	189	49.0	628	2 Q8UWD2	Q8UWD2 brachydantio

32	189	49.0	647	2 Q7T0K2	Q7T0K2 brachydantio
33	189	49.0	654	2 Q6ZM93	Q6ZM93 brachydantio
34	185	47.9	346	2 Q81S31	Q81S31 bombyx mori
35	185	47.9	346	2 Q968T8	Q968T8 bombyx mori
36	185	47.9	589	2 Q9ESB8	Q9ESB8 rat1us norv
37	185	47.9	589	2 Q9QZC6	Q9QZC6 rat1us norv
38	184	47.7	589	2 Q6P6S1	Q6P6S1 rat1us norv
39	184	47.7	612	1 BIR2 MOUSE	Q62210 mus musculu
40	183	47.4	534	2 Q81Z20	Q81Z20 homo sapien
41	183	47.4	604	2 Q6DDY3	Q6DDY3 xenopus lae
42	183	47.4	618	1 BIR2 HUMAN	Q13490 homo sapien
43	181	46.9	604	2 Q6GLD7	Q6GLD7 xenopus tro
44	180	46.6	263	2 Q80SF4	Q80SF4 hyphantria
45	180	46.6	283	2 Q80LX8	Q80LX8 adoxophyes

ALIGNMENTS

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RESULT 1
BIR4 RAT          STANDARD;          PRT;          496 AA.
ID BIR4 RAT
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP) (RIAP-3).
GN Name=Birc4; Synonyms=Api3, XIap;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC -1- (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS825, these interactions
CC -1- inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS825 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB033366; BAA85304.1; -
CC HSSP; P98170; 1151.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS01543; BIR_REPEAT_2; 3.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC AP00089; Repeat; Zinc-finger.
CC REPEAT 26 BIR 1.

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FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-type.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query March 94.8%; Score 366; DB 1; Length 496;
Best Local Similarity 93.9%; Pred. No. 4.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWTWISVNNKQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPMDQHAKEY 60
DB YDARIIVFTGWTWISVNNKQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPMDQHAKEY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 2
Q9ESFO PRELIMINARY; PRT; 496 AA.
ID Q9ESFO
AC Q9ESFO;
DT 01-MAR-2001 (TRENBLREL 16; Created)
DT 01-MAR-2001 (TRENBLREL 16; Last sequence update)
DT 01-JUN-2003 (TRENBLREL 24; Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes.";
RL BMC Genomics 3:5-5(2002).
DR EMBL; AF183429; AACG22969.1; -.
DR HSP; P98170; I151.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR SMART; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query March 94.8%; Score 366; DB 2; Length 496;
Best Local Similarity 93.9%; Pred. No. 4.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVFTGWTWISVNNKQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPMDQHAKEY 60
DB YDARIIVFTGWTWISVNNKQLARAGFYALGEGDKVYCFHCGGGLTDWKPSEDPMDQHAKEY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 3
BIR4_HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9NQ14;
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
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DT 25-OCT-2004 (Rel. 45; Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP-like protein) (HILP).
GN Name=BIRC4; Synonyms=API3, XIAP;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191; DOI=10.1038/379349a0;
RA Llaston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckert C.S., Nava V.E., Gedrick R.W., Clem R.J., van Dongen J.L.,
RA Giffillan M.C., Shields H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors.";
RL EMBO J. 15:2685-2694(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Graham D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplanton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshynski S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Maltay S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442; DOI=10.1038/40901;
RA Devereux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
RL Nature 388:300-304(1997).
RN [6]
RP NOTAGENSIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410; DOI=10.1074/jbc.M109891200;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "Htraz promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins.";
RL J. Biol. Chem. 277:445-454(2002).
RN [7]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637; DOI=10.1038/35050006;
```

RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
 RA Herrmann J., Wu J.C., Pesik S.W.,
 RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
 RT domain.";
 RL Nature 408:1004-1008 (2000).
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Ubiquitous, except peripheral blood
 CC leukocytes.
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
 CC and -7, while the third BIR is involved in caspase-9 inhibition.
 CC The interactions with SMAC and PRSS25 are mediated by the second
 CC and third BIR domains.
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U45880; AAC50373.1; -;
 DR EMBL: U32974; AAC50518.1; -;
 DR EMBL: AL121601; CAB95312.1; -;
 DR EMBL: BC032729; AAH32729.1; -;
 DR PIR: S69544; S69544.
 DR PDB: 1C9Q; NMR; A=124-240.
 DR PDB: 1F9X; NMR; A=237-356.
 DR PDB: 1G3F; NMR; A=240-356.
 DR PDB: 1G73; X-ray; C/D=238-358.
 DR PDB: 1I30; X-ray; E/F=120-240.
 DR PDB: 1I40; X-ray; C/D=120-260.
 DR PDB: 1I51; X-ray; E/F=124-240.
 DR PDB: 1KWC; X-ray; C/D=124-242.
 DR PDB: 1NW9; X-ray; A=253-350.
 DR GeneW: HGNC:592; BIRC4.
 DR H-invDB: HIX0017033; -;
 DR MIM: 300079; -;
 DR GO: GO:0005829; C:cytosol; TAS.
 DR GO: GO:0043027; F:caspase inhibitor activity; IDA.
 DR GO: GO:0006916; F:anti-apoptosis; TAS.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR002097; Profilin.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00236; BIR; 3.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR 3D-structure: Apoptosis; Repeat; Thiol protease inhibitor;
 KM Zinc-finger.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 265 330 BIR 3.
 FT ZN_RING 450 485 RING-type.
 FT MUTAGEN 148 148 D->A: Reduced interaction with PRSS25;
 FT MUTAGEN 259 259 N->D: Reduced interaction with PRSS25;
 FT MUTAGEN 310 310 W->R: Reduced interaction with PRSS25;
 FT MUTAGEN 214 214 when associated with S-314.
 FT MUTAGEN 214 D->S: Reduced interaction with PRSS25.
 FT MUTAGEN 314 314 associated with A-148.
 FT MUTAGEN E->S: Decreased interaction with SMAC and

FT FT with PRSS25. Decreases interaction with
 FT PRSS25; when associated with D-259 or A-
 FT 310.
 FT S -> C (in Ref. 1).
 FT Q -> P (in Ref. 2).
 FT
 FT CONFLICT 162 162
 FT CONFLICT 423 423
 FT TURN 128 130
 FT TURN 132 133
 FT TURN 136 142
 FT TURN 143 144
 FT STRAND 148 148
 FT HELIX 150 152
 FT TURN 153 153
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 Query Match 94.8%; Score 366; DB 1; Length 497;
 Best Local Similarity 95.5%; Pred. NO. 5e-35; Index 0; Gaps 0;
 Matches 63; Conservative 1; Mismatches 2;
 QY 1 YEARIVTFTWISVVKQQLARAGFYALGEGDYKCFHCGGLTDMKPSDPMDOHAKCY 60
 DB 265 YEARIPTFGTWISVVKQQLARAGFYALGEGDYKCFHCGGLTDMKPSDPMDOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 4
 Q9EQ04 PRELIMINARY; PRT; 501 AA.
 AC Q9EQ04;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Ovary;

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RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL: AF304334; AAC41193.1; -.
DR HSPSP; P98170; 1151.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART; SM00184; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69F2E0C8CD CRC64;

Query Match 94.8%; Score 366; DB 2; Length 501;
Best Local Similarity 93.9%; Pred. No. 5e-35; Indels 0; Gaps 0;
Matches 64; Conservative 3; Mismatches 1;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
DB 264 YDARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 5
Q9E005 PRELIMINARY; PRT; 501 AA.
AC Q9E005;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL: AF304333; AAC41192.1; -.
DR HSPSP; P98170; 1151.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56548 MW; 0973BFB28B81C5A0 CRC64;

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Query Match 93.5%; Score 361; DB 2; Length 501;
Best Local Similarity 92.4%; Pred. No. 2e-34;
Matches 61; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKCY 60
DB 264 YDARIYFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 6
BIR4 MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60985; O08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN Name=Birc4; Synonyms=Alpa, Ap13, Miha, Xiap;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=8643514; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.B.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS825; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS825 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSPSP; P98170; 1151.
DR MGD; MGI:107572; Birc4.
DR GO: GO:0001719; P:inhibition of caspase activation; IDA.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NCV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC039318; AAI39318.1; -
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR; 1.
DR SMART: SM00238; BIR; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PSS0143; BIR_REPEAT_2; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 236 AA; 27077 MW; DFB8350311PDAFBC CRC64;

Query Match 86.5%; Score 334; DB 2; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.5e-31;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWISVVKQELARAGFYALSGDRKVCFCGGLTDMKPSBDDPWDAKCY 60
Db 4 YEARIYFTGWISVVKQELARAGFYALSGDRKVCFCGGLTDMKPSBDDPWDAKCY 63
Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 9
061PYL
ID 061PYL PRELIMINARY; PRT; 338 AA.
AC 061PYL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE BIRC8 protein.
GN Name=BIRC8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko V., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC071665; AAH71665.1; -
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PSS0143; BIR_REPEAT_2; 2.
DR PROSITE: PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 338 AA; 38622 MW; DC17979CF92E4DF CRC64;

Query Match 86.5%; Score 334; DB 2; Length 338;
Best Local Similarity 81.8%; Pred. No. 2.2e-31;
Matches 54; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIYFTGWISVVKQELARAGFYALSGDRKVCFCGGLTDMKPSBDDPWDAKCY 60
Db 106 YEARIYFTGWISVVKQELARAGFYALSGDRKVCFCGGLTDMKPSBDDPWDAKCY 165
Qy 61 PGCKYL 66
Db 166 PGCKYL 171

RESULT 10
BIR8_PANTR
ID BIR8_PANTR STANDARD; PRT; 236 AA.
AC 095W72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonyms=ILP2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1126/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Prating A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (by
CC similarity).
CC -1- SUBUNIT: Binds to caspase-9 (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Inhibitor of apoptosis protein 3.
GN Name=IAP3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF451854; AL47170.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0006916; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00997; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Meta-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56C86119BC CRC64;
SO Query Match 72.3%; Score 279; DB 2; Length 493;
Best Local Similarity 71.2%; Pred. No. 1.2e-24;
Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISYVNSEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 264 YERRIQFLAMITPVNKEHLAEGFYSTGNDHYVCHCGGLQEMKENDPMDQHAKMF 323

QY 61 PGCKYL 66
DB 324 PGCKFL 329

RESULT 14
Q8MMY4 PRELIMINARY; PRT; 109 AA.
AC Q8MMY4;
DT 01-MAR-2002 (TEMBLrel. 20, last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, last sequence update)
DE 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN Name=XIAP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AL66179.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:000622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213DE6D CRC64;
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Query Match 66.8%; Score 258; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 8e-23;
Matches 44; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISYVNSEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 48
DB 57 YEARIYFTGWISYVNSEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKMF 104

RESULT 15
Q6DBV7 PRELIMINARY; PRT; 322 AA.
AC Q6DBV7;
DT 25-OCT-2004 (TEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, last sequence update)
DE 25-OCT-2004 (TEMBLrel. 28, last sequence update)
DE Hypothetical protein.
OS Brachydanio rerio (Zedrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussit T.B., Tohyiuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078344; AAH78344.1; -.
DR GO; GO:000622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR01370; Prot_inh_132_IAP.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 322 AA; 36412 MW; F9562546FA200CDF CRC64;

Query Match 54.9%; Score 212; DB 2; Length 322;
Best Local Similarity 51.5%; Pred. No. 7.3e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIYFTGWISYVNSEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMDOHAKCY 60
DB 229 FEGRLDSFKGRHPIDPRLIARAGFYSTGBODRVNCFRCGGVAKAMPDEDPWEEHARRY 288

QY 61 PGCKYL 66
DB 289 PGCSFL 294
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RESULT 16
ID 08UHM2 PRELIMINARY; PRT; 405 AA.
AC 08UHM2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Xlap.
GN Name=birc4;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Euarystota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Itohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Itohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF439767; AL32047.1; -.
DR HSSP; P98170; I130.
DR ZFIN; ZDB-GENE-030825-7; birc4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0089; ZF_RING_2; 1.
DR Meta-binding; Zinc; Zinc-finger.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366342D83BECAB CRC64;

Query Match 54.9%; Score 212; DB 2; Length 405;
Best Local Similarity 51.5%; Pred. No. 9.2e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKFCFGGGLTDWKPSSDPMDOHAKY 60
DB 229 FEGRLDSFKGRQHIDPERLARAGFYSTGEGDVMCFRCGGGVKAMPDDEDPMEHARHY 288
DB 289 PGCSFL 294

QY 61 PGCKYL 66
DB 289 PGCSFL 294

RESULT 17
ID 07SKU1 PRELIMINARY; PRT; 415 AA.
AC 07SKU1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Birc4 protein (Fragment).
GN Name=birc4;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Euarystota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toohilyukl S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Straubeberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BC05246; AAH5246.1; -.
DR HSSP; P98170; I130.
DR ZFIN; ZDB-GENE-030825-7; birc4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_1nh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0089; ZF_RING_2; 1.
DR Meta-binding; Zinc; Zinc-finger.
KW NON TER
SQ SEQUENCE 415 AA; 46788 MW; D9B82B448ADDC92 CRC64;

Query Match 54.9%; Score 212; DB 2; Length 415;
Best Local Similarity 51.5%; Pred. No. 9.4e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKFCFGGGLTDWKPSSDPMDOHAKY 60
DB 240 FEGRLDSFKGRQHIDPERLARAGFYSTGEGDVMCFRCGGGVKAMPDDEDPMEHARHY 289
DB 300 PGCSFL 305

QY 61 PGCKYL 66
DB 300 PGCSFL 305

RESULT 18
ID 06VTV9 PRELIMINARY; PRT; 280 AA.
AC 06VTV9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Choristoneura fumiferana defective nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=74660;
RN [1]
RP SEQUENCE FROM N.A.

```

RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138;
RA Li X., Barret J., Pang A., Klose R.J., Krell P.J., Arif B.M.;
RT "Characterization of an overexpressed spindle protein during a
RT baculovirus infection";
RL virology 268:56-67(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AY327402; AAC1688.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01262; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding: Zinc; Zinc-finger.
SQ SEQUENCE 280 AA; 32179 MW; CA8804614BFDPIAL CRC64;
Query Match 52.8%; Score 204; DB 2; Length 280;
Best Local Similarity 51.5%; Pred. No. 5.7e-16;
Matches 34; Conservative 14; Mismatches 16; Indels 2; Gaps 1;
QY 3 ARIVFGTWYSVVK--EQIARAGFYALGSGDKVCFHCGSGGLTMRPSEDPMDQAKCY 60
DB 115 ARKTFPDMVSLKQKPEQLAELAGFYTGKGRKCKHCGGLKDWESTDEPMENHARMF 174
QY 61 PGCKYL 66
DB 175 DRCYTV 180
RESULT 19
BIR3_HUMAN STANDARD; PRT; 604 AA.
ID BIR3_HUMAN
AC Q13489; Q16628; Q9HC27; Q9UP46;
DT 01-NOV-1997 (Ref. 35, Created)
DT 01-NOV-1997 (Ref. 35, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis
DE protein 1) (IAP homolog C) (C-IAP2) (TNFR2-TRAF signaling complex
GN Name:BIRC3; Synonyms:API2, IAP1, MIRC;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eularchia; Primates; Catarrhini; Homnidae; Homo.
OX Mammalia; Eularchia; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9618127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
RX Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9619249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Tamai K., Lefebvre C., Bald S., Chertou-Horvat G.,
RA Farahani R., McLean M., Ikeda Y., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes";

RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal liver;
RX MEDLINE=96209883; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Torre-Veale A.J., Fontijn R.D., Van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes";
RL Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin J.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wallat S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Vellaton D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fillion J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RX DOI=10.1002/1098-2264(2000)999<:AID-GC1036>3.0.CO;2-I;
RA Baens M., Steys A., Dierlam J., De Wolf-Peters C., Marynen P.;
RT "Structure of the MTR gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RL B-cell lymphomas of MALT type";
CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form an heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Highly expressed in fetal lung, and kidney. In
CC the adult, expression is mainly seen in lymphoid tissues,
CC including spleen, thymus and peripheral blood lymphocytes.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC3.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

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CC      WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BIRC3ID239.html".
CC      -----
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CC      -----
DR      EMBL; LA9432; AAC41943.1; -
DR      EMBL; U45878; AAC50371.1; -
DR      EMBL; U37546; AAC50507.1; -
DR      EMBL; AF070674; AAC83232.1; -
DR      EMBL; BC037420; AAC37420.1; -
DR      EMBL; AF178945; AAC09369.1; -
DR      PIR; S68449; S68449.
DR      HSP; Q13490; IOBH.
DR      Genew; HGNC:591; BIRC3.
DR      MIM; 601721; -
DR      GO; GO:0005515; F:protein binding; NAS.
DR      GO; GO:0006916; P:anti-apoptosis; TAS.
DR      GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR      InterPro; IPR001370; BIR.
DR      InterPro; IPR001315; CARD.
DR      InterPro; IPR011029; DEATH_1ike.
DR      InterPro; IPR001841; Znf_ring.
DR      Pfam; PF00653; BIR; 3.
DR      Pfam; PF00619; CARD; 1.
DR      Pfam; PF00097; zf-C3HC4; 1.
DR      SMART; SM00238; BIR; 3.
DR      SMART; SM00114; CARD; 1.
DR      SMART; SM00184; RING; 1.
DR      PROSITE; PS01282; BIR_REPEAT_1; 3.
DR      PROSITE; PS50143; BIR_REPEAT_2; 3.
DR      PROSITE; PS50209; CARD; 1.
DR      PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE; PS50089; ZF_RING_2; 1.
DR      Apoptosis; Chromosomal translocation; Repeat; Zinc-finger.
DR      REPEAT; 29
DR      REPEAT; 169
DR      REPEAT; 255
DR      REPEAT; 322
DR      DOMAIN; 439
DR      DOMAIN; 529
DR      ZN_FING; 557
DR      SIB; 442
DR      SIB; 443
DR      FT; CONFLICT; 18
DR      FT; CONFLICT; 119
DR      FT; CONFLICT; 153
DR      FT; CONFLICT; 163
DR      FT; CONFLICT; 165
DR      FT; CONFLICT; 191
DR      FT; CONFLICT; 364
DR      FT; CONFLICT; 552
DR      SQ; SEQUENCE; 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;

Query Match      51.3%; Score 198; DB 1; Length 604;
Best Local Similarity 55.9%; Pred. No. 6,4e-15;
Matches 39; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY      1 YEARTVFGTWIYS--VNEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDQHAQ 58
Db      255 HAARFKTFEFWMPSSVLVNPQQLASAGFYVYGNSDVACFCDDGLRCMESGDDPDWQHAQ 314
QY      59 CYPGCKYL 66
Db      315 WPRCEYL 322

RESULT 20
Q6E7G7 PRELIMINARY; PRT; 287 AA.
AC      Q6E7G7;

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DT      25-OCT-2004 (TEMBLrel. 28, Created)
DT      25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE      IAP-3.
OS      Anticarsa gemmatilis nuclear polyhedrosis virus (AgMNPV).
OC      Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC      Nucleopolyhedrovirus.
OX      NCBI_TaxID=31507;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Carpes M.P., Castro M.E., Soares E.F., Villela A.G., Plinedo F.J.,
RA      Ribeiro B.M.;
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY525121; AAS92269.1; -
DR      GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR      GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR      GO; GO:0008270; F:zinc ion binding; IEA.
DR      GO; GO:0006316; P:anti-apoptosis; IEA.
DR      GO; GO:0016567; P:protein ubiquitination; IEA.
DR      InterPro; IPR001370; Prot_1h_132_IAP.
DR      InterPro; IPR001841; Znf_ring.
DR      Pfam; PF00653; BIR; 2.
DR      SMART; SM00238; BIR; 2.
DR      PROSITE; PS01282; BIR_REPEAT_1; 2.
DR      PROSITE; PS50143; BIR_REPEAT_2; 2.
DR      PROSITE; PS50089; ZF_RING_2; 1.
SQ      SEQUENCE 287 AA; 32620 MW; 20F3A7F0C11C4C2B CRC64;

Query Match      50.8%; Score 196; DB 2; Length 287;
Best Local Similarity 50.0%; Pred. No. 5.2e-15;
Matches 33; Conservative 14; Mismatches 17; Indels 2; Gaps 1;

QY      3 ARIVTFGTWIVSYNK--EQIARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDQHAQ 60
Db      127 ARKTFEDMPLSLKQRPQLAEAGFYTGKDKVKCFDGGGLKDMANDEPHEHARWF 166
QY      61 PGCKYL 66
Db      187 DRCSFV 192

RESULT 21
PIAP PIG STANDARD; PRT; 358 AA.
AC      062610;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Putative inhibitor of apoptosis.
GN      Name=PIAP;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE=Adip;
RX      MEDLINE=98162622; PubMed=9501011; DOI=10.1006/bhrc.1998.8185;
RA      Stenlik C., de Martin R., Binder B.R., Lipp J.;
RT      "Cytokine induced expression of porcine inhibitor of apoptosis protein
RT      (Iap) family member is regulated by NF-kappa B.";
RL      Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC      -1- SIMILARITY: Belongs to the IAP family.
CC      -1- SIMILARITY: Contains 2 BIR repeats.
CC      -1- SIMILARITY: Contains 1 CARD domain.
CC      -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC      -----
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC EMBL: U79142; AAC39171.1; -.
DR PIR: JC5964; JC5964.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH_1like.
DR InterPro: IPR01841; Znf_ring.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Apoptosis; Repeat; Zinc-finger.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_RING 311 346 RING-type.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 50.8%; Score 196; DB 1; Length 358;
Best Local Similarity 54.4%; Pred. No. 6.6e-15;
Matches 37; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIYFGTWIY--VYNKQILARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQAK 58
Db 90 YAAKFKTFCWPPSSIPVHPQLASAGFYVMGSHSDVXCFCDCGLRCWESGDDPFWVHAK 149
RT "Genetic variation among chicken lines and mammalian species in
specific genes."
RL Poul. Sci. 80:284-288 (2001).
DR EMBL: AP221082; AAF35319.1; -.
DR HSSP: Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT NON_TER 195 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

RESULT 22
ID Q9IA70 PRELIMINARY; PRT; 195 AA.
AC Q9IA70;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-bred Leghorn; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes."
RL Poul. Sci. 80:284-288 (2001).
DR EMBL: AP221082; AAF35319.1; -.
DR HSSP: Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT NON_TER 195 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 49.7%; Score 192; DB 2; Length 195;
Best Local Similarity 52.9%; Pred. No. 1.1e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIYFGTW--IYSVNEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQAK 58
Db 116 HEARKVTFINWPRIPVQPEQLADAGFYVGRNDVXCFCDCGLRCWESGDDPFWIEHAK 175
RT "Genetic variation among chicken lines and mammalian species in
specific genes."
RL Poul. Sci. 80:284-288 (2001).
DR EMBL: AP221082; AAF35320.1; -.
DR HSSP: Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT NON_TER 197 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 49.7%; Score 192; DB 2; Length 197;
Best Local Similarity 52.9%; Pred. No. 1.1e-14;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIYFGTW--IYSVNEQLARAGFYALGEGDKYKCFHCGGGLTDMKSEDPMDQAK 58
Db 117 HEARKVTFINWPRIPVQPEQLADAGFYVGRNDVXCFCDCGLRCWESGDDPFWIEHAK 176
RT "Genetic variation among chicken lines and mammalian species in
specific genes."
RL Poul. Sci. 80:284-288 (2001).
DR EMBL: AP221082; AAF35320.1; -.
DR HSSP: Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT NON_TER 197 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

RESULT 24
ID Q9ESB9 PRELIMINARY; PRT; 602 AA.
AC Q9ESB9;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

QY 59 CYGCKYL 66
 Db 322 WFPCEYL 329

RESULT 26

IAP3_NPVOP STANDARD; PRT; 268 AA.
 ID IAP3_NPVOP
 AC P41437;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Apoptosis inhibitor 3 (IAP-3).
 GN Name=IAP3; Synonym=IAP;
 OS Orygia pseudotsugata multicausid polyhedrosis virus (OpMNVP).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 CX NCBI_TaxID=164623;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187094; PubMed=8139034;
 RA Birnbaum M.J., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
 RT encoding a polypeptide with Cys/His sequence motifs.";
 RL J. Virol. 68:2521-2528(1994).
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126251; DOI=10.1006/viro.1997.8448;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
 RT polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 RN RN
 RP INTERACTION WITH HUMAN PDCL3.
 RX PubMed=15371430; DOI=10.1074/jbc.M409623200;
 RA Wilkinson J.C., Richter B.W.M., Wilkinson A.S., Burrestein E.,
 RA Rumble J.M., Ballin B., Duckett C.S.;
 RT "VIAF, a conserved inhibitor of apoptosis (IAP) interacting factor
 RT that modulates caspase activation.";
 RL J. Biol. Chem. 279:0-0(2004).
 CC -1- FUNCTION: Acts by blocking cellular apoptosis rather than by
 CC preventing viral stimulation of apoptosis.
 CC -1- SUBUNIT: Interacts with human PDCL3.
 CC -1- SIMILARITY: Contains 2 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC CC
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 CC -----
 CC EMBL: L22564; AAB02610.1; -;
 CC EMBL: U75930; AAC59034.1; -;
 CC PIR: A53989; A53989.
 CC HSSP: Q24306; IJDA.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00653; BIR. 2.
 CC Pfam: PF00097; ZF-C3HC4. 1.
 CC SMART: SM00238; BIR. 2.
 CC SMART: SM00184; RING. 1.
 CC PROSITE: PS01282; BIR_REPEAT_1; 2.
 CC PROSITE: PS0143; BIR_REPEAT_2; 2.
 CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE: PS00089; ZF_RING_2; 1.
 CC Apoptosis; Repeat; zinc-finger.
 CC REPEAT 18 84 BIR 1.
 CC REPEAT 111 178 BIR 2.

FT ZN RING 221 256 RING-type.
 SQ SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;
 Query Match 49.2%; Score 190; DB 1; Length 268;
 Best Local Similarity 48.5%; Pred. No. 2, 5e-14;
 Matches 32; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVFGTWISYVK--EQIARAGFYALGEGDKYKCFHCGGLTDWKPSEDPMDQNAKCY 60
 Db 113 ARIRTFEAWPRGKQRPBRLAEAGFFYTGGDKTRCFCCDGLKDWEPDDAPMGOHARWY 172

QY 61 PGCKYL 66
 Db 173 DRCEYV 178

RESULT 27

O6QXJ6 PRELIMINARY; PRT; 269 AA.
 ID O6QXJ6
 AC O6QXJ6;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE O6P53.
 GN Name=O6P53; IAP-1; ORENAMES=AgVp053;
 OS Agrotis segetum granulosis virus (AgV) (Agrotis segetum
 OC granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 CX NCBI_TaxID=10464;
 RN RN
 RP SEQUENCE FROM N.A.
 RA Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Yuhu S., Mei H.;
 RT "Agrotis segetum Granulosis Virus complete genome.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN RN
 RP SEQUENCE FROM N.A.
 RG Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Shi X.H., He M.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN RN
 RP SEQUENCE FROM N.A.
 RG Shanghai GeneCore Biotechnology Ltd;
 RA Xuilian A., Zhifang W., Bo W., Wei Z., Jianhong F., Chunsheng C.,
 RA Yuhu S., Mei H.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY522332; AAS82685.1; -;
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001370; Prot_inh_132_IAP.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00653; BIR. 2.
 DR SMART: SM00238; BIR. 2.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS0143; BIR_REPEAT_2; 2.
 DR PROSITE: PS00089; ZF_RING_2; 1.
 SQ SEQUENCE 269 AA; 31135 MW; C929C533465EBC51 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 269;
 Best Local Similarity 47.8%; Pred. No. 3, 4e-14;
 Matches 32; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVFGTWISYV--NKEQIARAGFYALGEGDKYKCFHCGGLTDWKPSEDPMDQNAKCY 59
 Db 115 ENRLEBSYKTMWPSIPLRPKELAAAGFYTGYSHDQVNCFCGGGLRDWKTGDDPMDQHARW 174


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Db          313 WPRCEYL 320

RESULT 30
Q804E2      PRELIMINARY;      PRT: 616 AA.
AC          Q804E2;
DT          01-JUN-2003 (TrEMBLrel. 24, Created)
DT          01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT          01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE          Inhibitor of apoptosis protein-1.
GN          Name=IAP-1;
OS          Ictalurus punctatus (Channel catfish).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC          Ictaluridae; Ictalurus.
OX          NCBI_TaxId=7998;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Praveen K., Leary J.H. III, Evans D.L., Jaseo-Friedmann L.;
RL          Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR          EMBL: AY184377; AAC24632.1; -.
DR          HSSP: Q13490; 10BH.
DR          GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR          GO: GO:0005515; F:protein binding; IEA.
DR          GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR          GO: GO:0008270; F:zinc ion binding; IEA.
DR          GO: GO:0006916; P:anti-apoptosis; IEA.
DR          GO: GO:0016567; P:protein ubiquitination; IEA.
DR          GO: GO:0042881; P:regulation of apoptosis; IEA.
DR          InterPro: IPR001315; CARD.
DR          InterPro: IPR011029; DEATH_1like.
DR          InterPro: IPR001370; Prot_inh_132_IAP.
DR          InterPro: IPR001841; Znf_Fing.
DR          Pfam: PF00653; BIR_3.
DR          Pfam: PF00619; CARD; 1.
DR          Pfam: PF00097; zf-C3HC4; 1.
DR          SMART: SM00238; BIR; 3.
DR          SMART: SM00184; CARD; 1.
DR          SMART: SM00184; RING; 1.
DR          PROSITE: PS01282; BIR_REPEAT_1; 2.
DR          PROSITE: PSS0143; BIR_REPEAT_2; 3.
DR          PROSITE: PSS0209; CARD; 1.
DR          PROSITE: PSS0089; ZF_RING_2; 1.
DR          Metal-binding; Zinc; Zinc-finger.
KM          Metab-binding; Zinc; Zinc-finger.
SQ          SEQUENCE 616 AA; 69546 MW; D1389D915C6B256 CRC64;

Query Match          49.0%; Score 189; DB 2; Length 616;
Best Local Similarity 50.7%; Pred. No. 7.7e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY          2 EARIVTFGTW--IYSVNKEQLARAGFYALGEGDKVKVFCGGLITWPKSEDPMDQAKC 59
DB          270 EERLLTFVWMPRIPIRPDPQLAKAGFYVGRNDVVKCFCCDGLRCWESGDDPWEVHAKW 329
QY          60 YPGCKYL 66
DB          330 FPRCEYL 336

RESULT 31
Q80WMD2     PRELIMINARY;      PRT: 628 AA.
AC          Q80WMD2;
DT          01-MAR-2002 (TrEMBLrel. 20, Created)
DT          01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT          01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE          Iap1.
GN          Name=birc3; Synonyms=iap1;
GN          Brachydanio rerio (Zebrafish) (Danio rerio).
OS          Brachydanio rerio (Zebrafish); Craniata; Vertebrata; Euteleostomi;
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC          Ictaluridae; Ictalurus.
OX          NCBI_TaxId=7998;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Praveen K., Leary J.H. III, Evans D.L., Jaseo-Friedmann L.;
RL          Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR          EMBL: AY184377; AAC24632.1; -.
DR          HSSP: Q13490; 10BH.
DR          GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR          GO: GO:0005515; F:protein binding; IEA.
DR          GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR          GO: GO:0008270; F:zinc ion binding; IEA.
DR          GO: GO:0006916; P:anti-apoptosis; IEA.
DR          GO: GO:0016567; P:protein ubiquitination; IEA.
DR          GO: GO:0042881; P:regulation of apoptosis; IEA.
DR          Pfam: PF00653; BIR; 3.
DR          Pfam: PF00619; CARD; 1.
DR          Pfam: PF00097; zf-C3HC4; 1.
DR          SMART: SM00238; BIR; 3.
DR          SMART: SM00184; CARD; 1.
DR          SMART: SM00184; RING; 1.
DR          PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR          PROSITE: PSS0143; BIR_REPEAT_2; 3.
DR          PROSITE: PSS0209; CARD; 1.
DR          PROSITE: PSS0089; ZF_RING_2; 1.
DR          Metal-binding; Zinc; Zinc-finger.
KM          Metab-binding; Zinc; Zinc-finger.
SQ          SEQUENCE 628 AA; 70098 MW; 5B68CEBA87C8A95 CRC64;

Query Match          49.0%; Score 189; DB 2; Length 628;
Best Local Similarity 50.7%; Pred. No. 7.9e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY          2 EARIVTFGTW--IYSVNKEQLARAGFYALGEGDKVKVFCGGLITWPKSEDPMDQAKC 59
DB          280 EERLLTFVWMPRIPIRPDPQLAKAGFYVGRNDVVKCFCCDGLRCWESGDDPWEVHAKW 339
QY          60 YPGCKYL 66
DB          340 FPRCEYL 346

RESULT 32
Q77OK2      PRELIMINARY;      PRT: 647 AA.
AC          Q77OK2;
DT          01-OCT-2003 (TrEMBLrel. 25, Created)
DT          01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT          01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE          Inhibitor of apoptosis protein.
GN          Name=birc3;
OS          Brachydanio rerio (Zebrafish) (Danio rerio).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC          Cyprinidae; Danio.
OX          NCBI_TaxId=7955;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Ems K.M., Valdimarsson G.;
RL          Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR          EMBL: AY247786; AAP04483.1; -.
DR          HSSP: P98170; 1130.
DR          ZFIN: ZDB-GENE-030825-6; birc3.
```

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OC          Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC          Cyprinidae; Danio.
OX          NCBI_TaxId=7955;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=20373792; PubMed=10917738;
RA          Inohara N., Nunez G.;
RT          "Genes with homology to mammalian apoptosis regulators identified in
RT          zebrafish."
RL          Cell Death Differ. 7:509-510(2000).
RN          [2]
RP          SEQUENCE FROM N.A.
RA          Inohara N., Nunez G.;
RL          Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR          EMBL: AF442500; AAL33679.1; -.
DR          HSSP: Q13490; 10BH.
DR          ZFIN: ZDB-GENE-030825-6; birc3.
DR          GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR          GO: GO:0005515; F:protein binding; IEA.
DR          GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR          GO: GO:0008270; F:zinc ion binding; IEA.
DR          GO: GO:0006916; P:anti-apoptosis; IEA.
DR          GO: GO:0016567; P:protein ubiquitination; IEA.
DR          GO: GO:0042881; P:regulation of apoptosis; IEA.
DR          Pfam: PF00653; BIR; 3.
DR          Pfam: PF00619; CARD; 1.
DR          Pfam: PF00097; zf-C3HC4; 1.
DR          SMART: SM00238; BIR; 3.
DR          SMART: SM00184; CARD; 1.
DR          SMART: SM00184; RING; 1.
DR          PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR          PROSITE: PSS0143; BIR_REPEAT_2; 3.
DR          PROSITE: PSS0209; CARD; 1.
DR          PROSITE: PSS0089; ZF_RING_2; 1.
DR          Metal-binding; Zinc; Zinc-finger.
KM          Metab-binding; Zinc; Zinc-finger.
SQ          SEQUENCE 628 AA; 70098 MW; 5B68CEBA87C8A95 CRC64;

Query Match          49.0%; Score 189; DB 2; Length 628;
Best Local Similarity 50.7%; Pred. No. 7.9e-14;
Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY          2 EARIVTFGTW--IYSVNKEQLARAGFYALGEGDKVKVFCGGLITWPKSEDPMDQAKC 59
DB          280 EERLLTFVWMPRIPIRPDPQLAKAGFYVGRNDVVKCFCCDGLRCWESGDDPWEVHAKW 339
QY          60 YPGCKYL 66
DB          340 FPRCEYL 346

RESULT 33
Q77OK2      PRELIMINARY;      PRT: 647 AA.
AC          Q77OK2;
DT          01-OCT-2003 (TrEMBLrel. 25, Created)
DT          01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT          01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE          Inhibitor of apoptosis protein.
GN          Name=birc3;
OS          Brachydanio rerio (Zebrafish) (Danio rerio).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC          Cyprinidae; Danio.
OX          NCBI_TaxId=7955;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Ems K.M., Valdimarsson G.;
RL          Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR          EMBL: AY247786; AAP04483.1; -.
DR          HSSP: P98170; 1130.
DR          ZFIN: ZDB-GENE-030825-6; birc3.
```

DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006916; F:anti-apoptosis; IEA.
 DR GO: GO:0016567; F:protein ubiquitination; IEA.
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR011029; DEATH like.
 DR InterPro: IPR001370; ProtInh_I32_IAP.
 DR InterPro: IPR001841; Znf_Fing.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 647 AA; 72183 MW; 88DBBAFE92718FA9 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 647;
 Best Local Similarity 50.7%; Pred. No. 8.1e-14;
 Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSEDPWDQIAKC 59
 DB EERLITFTVWPSRIPIVRPDQAKAGFYVGRNDVVCFCDDGGLRCWESGDDPWVEHAKW 358
 QY 60 YPGCKYL 66
 DB 359 FPRCEYL 365

RESULT 33

Q6ZM93 PRELIMINARY; PRT; 654 AA.
 AC Q6ZM93
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE St: bz1p1.6.2 (Baculoviral IAP repeat-containing 3).
 GN Nameb1rc3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_Taxid=7955;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Clark G.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC EMBL: AL627325; CAB47763.1; -
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; F:anti-apoptosis; IEA.
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR011029; DEATH like.
 DR InterPro: IPR001370; ProtInh_I32_IAP.
 DR InterPro: IPR001841; Znf_Fing.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 654 AA; 72995 MW; A12425D5E41A0359 CRC64;

Query Match 49.0%; Score 189; DB 2; Length 654;
 Best Local Similarity 50.7%; Pred. No. 8.2e-14;
 Matches 34; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSEDPWDQIAKC 59
 DB EERLITFTVWPSRIPIVRPDQAKAGFYVGRNDVVCFCDDGGLRCWESGDDPWVEHAKW 365
 QY 60 YPGCKYL 66
 DB 366 FPRCEYL 372

RESULT 34

O8IS31 PRELIMINARY; PRT; 346 AA.
 AC O8IS31
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Inhibitor of apoptosis protein.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Lepidoptera; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OC NCBI_Taxid=7091;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Yang G., Wang L., Wu X.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY155274; AAN46650.1; -
 DR HSSP: Q24306; 1040.
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; F:anti-apoptosis; IEA.
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR001370; ProtInh_I32_IAP.
 DR InterPro: IPR001841; Znf_Fing.
 DR Pfam: PF00653; BIR; 2.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 2.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 346 AA; 36849 MW; 5450EB75F56A8486 CRC64;

Query Match 47.9%; Score 185; DB 2; Length 346;
 Best Local Similarity 47.0%; Pred. No. 1.3e-13;
 Matches 31; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVTGTW--IYSVVKQLARAGFYALGEGDKYKCFHCGGGLTDWKPSEDPWDQIAKC 60
 DB ARLATFDWPRCQRKRPBELAAGFYVGGDKTKCFYCDGGLKDWESDDPWVEHARWF 243
 QY 61 PGCKYL 66
 DB 244 DRCAVY 249

RESULT 35

O968T8 PRELIMINARY; PRT; 346 AA.
 AC O968T8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DR 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240184; PubMed=11341966; DOI=10.1016/S0167-4889(00)00105-1;
RA Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) from Bombyx mori.";
RL Blochim. Biophys. Acta 1499:191-198(2001).
DR EMBL; AF281073; AAK57560.1; -.
DR HSSP; Q24306; 104Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00184; RING; 1.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PSS01282; BIR_REPEAT_1; 2.
DR PROSITE; PSS0143; BIR_REPEAT_2; 2.
DR PROSITE; PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CF6C6468894C69 CRC64;

Query Match 47.9%; Score 185; DB 2; Length 346;
Best Local Similarity 47.0%; Pred. No. 1.3e-13;
Matches 31; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 3 ARIVFGTWIYSVK--EQARAGFYALGEGDKVCKFHCGGLTDMKPSDPMDOHAKY 60
DB 184 ARLATFDWMRRMRQKPEELAEAGFFVTGGQDKKCFYCGGLKDWESDVPMEQHARWF 243
QY 61 PGCKYL 66
DB 244 DRCAVY 249

RESULT 36
Q9ESB8 PRELIMINARY; PRT; 589 AA.
AC Q9ESB8;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneljuk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes.";
RL BMC Genomics 3:5-5(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF183431; AAG22971.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.

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```

DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011028; DEATH_1like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS01282; BIR_REPEAT_1; 3.
DR PROSITE; PSS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0209; CARD; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 47.9%; Score 185; DB 2; Length 589;
Best Local Similarity 51.5%; Pred. No. 2.2e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYFGTWIYS--VNNEQLARAGFYALGEGDKVCKFHCGGLTDMKPSDPMDOHAK 58
DB 241 HSARMSFTLWPSVVLQPEQLASAGFYVDNDVDVCKFCDCGLRCWBERGDDPMIEHAK 300
QY 59 CYPGCKYL 66
DB 301 WPRCEPL 308

RESULT 37
Q9QZC6 PRELIMINARY; PRT; 589 AA.
ID Q9QZC6;
AC Q9QZC6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22020585; PubMed=12023884; DOI=10.1042/BJ20011431;
RA Dong Z., Nishiyama Y., Yi X., Venkatchalam M.A., Denton M., Gu S.,
RA Li S., Qiang M.;
RT "Gene promoter of apoptosis inhibitory protein IAP2: identification of
RT enhancer elements and activation by severe hypoxia.";
RL Biochem. J. 364:413-421(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF190020; AAF04585.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH_1like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; ZF_C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.

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DR SMART, SM00184; RING, 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM Metal-binding; zinc; zinc-finger.
 SQ SEQUENCE 589 AA; 66777 MW; E6812FF63EA34142 CRC64;

Query Match 47.7%; Score 185; DB 2; Length 589;
 Best Local Similarity 51.5%; Pred. No. 2,2e-13;
 Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFGTWIYS--VNKEQLADAGFYALGEGDKVXCFHCGGLTDMKPSDEPMDQHA 58
 Db 241 HSNARMTFLYWPSSVLVQPEQLASAGFYVYDNDVVKCFCCDGLRCMEPDDPWIEHAK 300
 QY 59 CYPGCKYL 66
 Db 301 WFPRCERL 308

RESULT 38
 ID Q6P6S1 PRELIMINARY; PRT; 589 AA.
 AC Q6P6S1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Apoptosis inhibitor 2.
 GN Name=Ap12;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feinold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Mulhaby S.J.,
 RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzaniak M.I., Skolnik J., Skolnik J., Skolnik J., Skolnik J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Prostate;
 RC Strauberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC EMBL, BC062055; AAH62055.1;
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0005515; P:protein binding; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR GO; GO:0042961; P:regulation of apoptosis; IEA.
 DR InterPro; IPR001315; CARD.

DR InterPro; IPR011029; DEATH_1like.
 DR InterPro; IPR001370; Prot_inh_132_IAP.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00057; ZF-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM Metal-binding; zinc; zinc-finger.
 SQ SEQUENCE 589 AA; 66846 MW; 526BCBAA9052EF49 CRC64;

Query Match 47.7%; Score 184; DB 2; Length 589;
 Best Local Similarity 51.5%; Pred. No. 2,9e-13;
 Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFGTWIYS--VNKEQLADAGFYALGEGDKVXCFHCGGLTDMKPSDEPMDQHA 58
 Db 241 HSNARMTFLYWPSSVLVQPEQLASAGFYVYDNDVVKCFCCDGLRCMEPDDPWIEHAK 300
 QY 59 CYPGCKYL 66
 Db 301 WFPRCERL 308

RESULT 39
 ID BIR2_MOUSE STANDARD; PRT; 612 AA.
 AC 062210; 008864;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
 DE protein 2) (MIAP2) (MIAP-2).
 GN Name=Birc2; Synonyms=Birc3, Iap2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96128127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
 RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related
 RT to baculoviral inhibitor of apoptosis proteins";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98110590; PubMed=9441756; DOI=10.1006/geno.1997.5059;
 RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein
 RT 1 and 2 genes";
 RL Genomics 46:495-503(1997).
 CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
 CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
 CC form an heteromeric complex, which is then recruited to the tumor
 CC necrosis factor receptor 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
 CC inhibit apoptotic suppressor activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
 CC liver, skeletal muscle, kidney and testis.
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc domain.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announce/>
CC or send an email to license@ebi.ac.uk).

DR EMBL; L49433; AAC42078.1; -;
DR EMBL; U88909; AAC53532.1; -;
DR HSSP; Q13490; 10BH.
DR MGD; MGI:1197009; Birc3.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR01029; DEATH_1ike.
DR InterPro; IPR01841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Direct protein sequencing; Repeat; Zinc-finger.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-type.
FT CONFLICT 380 380 E -> K (in Ref. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 47.7%; Score 184; DB 1; Length 612;
Best Local Similarity 51.5%; Pred. No. 3e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFTWIS--VNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAK 58
DB 262 HSARLRFTLYMPSSVFPQPSQLASAGFYVGRNDVVKCFCCDGLRCWESGDDPWFHAK 321
QY 59 CYPCKXYL 66
DB 322 WPPRCFEL 329

RESULT 40

Q81220
ID O81220 PRELIMINARY; PRT; 534 AA.
AC O81220;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE PRD-interacting protein RBBP-36.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Pan 2.S.; Ao S.Z.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207599; AAN73272.1; -;
DR HSSP; Q13490; 10BH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR001315; CARD.

DR InterPro; IPR011029; DEATH_1ike.
DR InterPro; IPR001370; Prot_inh_132_1AP.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
SQ SEQUENCE 534 AA; 60366 MW; 0403170475BE0872 CRC64;

Query Match 47.4%; Score 183; DB 2; Length 534;
Best Local Similarity 51.5%; Pred. No. 3.5e-13;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIYVFTWIS--VNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSBDPMDQAK 58
DB 269 HAHMRFTFWMPSSVFPQPSQLASAGFYVGRNDVVKCFCCDGLRCWESGDDPWFHAK 328
QY 59 CYPCKXYL 66
DB 329 WPPRCFEL 336

Search completed: June 15, 2005, 17:39:35
Job time : 115.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:18:26 ; Search time 115 Seconds
(without alignment)
221.967 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIPTFTGWTIVSVNKEQL.....KPSHPWQHAKVPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	66	7	ADB61810 Human inh
2	389	100.0	110	8	ADP90805 Human XIA
3	389	100.0	236	5	ABG32418 X-linked
4	389	100.0	278	5	AAO20511 Protein o
5	389	100.0	497	2	AAW19581 Human apo
6	389	100.0	497	2	AAW69294 Human XIA
7	389	100.0	497	3	AAV59451 Human XIA
8	389	100.0	497	3	AAV99985 Human X-1
9	389	100.0	497	5	ABG65663 Human inh
10	389	100.0	497	5	ADB80961 RING-SH C
11	389	100.0	497	7	AD139804 Human inh
12	389	100.0	497	7	ADH74639 Human XIA
13	389	100.0	497	8	ADL70166 Human X c
14	389	100.0	497	8	ADP23982 PRO polyp
15	377	96.9	66	7	ADB61827 Rat inhib
16	368	94.6	496	2	AAW19745 Mouse inh
17	366	94.1	496	2	AAW19584 Mouse apo
18	366	94.1	496	2	AAW69297 Murine XI
19	366	94.1	496	5	ABG65666 Mouse inh
20	352	90.5	66	7	ADB61828 Mouse inh
21	352	90.5	496	6	ABP72157 Mouse inh
22	347	89.2	66	7	ADB61820 Human inh
23	347	89.2	236	7	AAV81440 Human TIA
24	347	89.2	236	4	AAE00365 Human IAP
25	347	89.2	236	5	AAU75066 Human tes

26	347	89.2	236	5	ABG32417 Inhibitor
27	347	89.2	464	5	AAU75747 Human inh
28	342.5	88.0	87	8	ADR44576 X-IAP BIR
29	341	87.7	236	4	AAE00366 Chimpanze
30	338	86.9	66	7	ADB61831 Gorilla i
31	338	86.9	236	4	AAE00367 Gorilla I
32	322	82.8	57	7	ADB61832 Unidentif
33	295	75.8	53	7	AD139821 Human NAI
34	287	73.8	66	7	ADB61829 Chicken I
35	273	70.2	151	5	ADK34975 Novel hum
36	255	65.6	52	7	ADB61830 Bovine in
37	216	55.5	68	7	ADB61833 Zebra fil
38	211	54.2	68	7	ADB61813 Human inh
39	211	54.2	442	8	ADOC6592 Human API
40	211	54.2	557	6	ABP72159 Inhibitor
41	211	54.2	604	2	AAW19582 Human apo
42	211	54.2	604	2	AAW19747 Human inh
43	211	54.2	604	2	AAW1546 Human c-I
44	211	54.2	604	2	AAW69295 Human HIA
45	211	54.2	604	2	AAV52703 Human cel

ALIGNMENTS

RESULT 1	ID	ADB61810	standard; protein; 66 AA.
XX	AC	ADB61810;	
XX	DT	04-DEC-2003 (first entry)	
XX	DE	Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.	
XX	XX	baculovirus inhibitor of apoptosis repeat domain; BIR domain;	
XX	KW	apoptosis pathway; embryonic development; viral pathogenesis; cancer;	
XX	KW	autoimmune disorder; neurodegenerative disease; apoptotic response;	
XX	KW	systemic lupus erythematosus; multiple sclerosis; viral infection;	
XX	KW	herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;	
XX	KW	HR23, CIAP2; HR23; CIAP1; RING zinc finger; caspase-3; caspase-7;	
XX	KW	caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;	
XX	KW	cervical cancer; uterine cancer; testicular cancer;	
XX	KW	small cell lung carcinoma; uterine cancer; renal cell carcinoma;	
XX	KW	Wilm's tumour; human; BIR 3 domain.	
XX	OS	Homo sapiens.	
XX	PN	W02003040172-A2.	
XX	PD	15-MAY-2003.	
XX	PF	12-NOV-2002; 2002W0-CA001738.	
XX	PP	09-NOV-2001; 2001US-0332300P.	
XX	PR	08-APR-2002; 2002US-0370934P.	
XX	XX	(AEGF-) AEGERA THERAPEUTICS INC.	
XX	PA		
XX	XX	Boudreaux A, Korneluk RG, La Casse E, Létour P,	
XX	XX	WPI; 2003-513532/48.	
XX	DR		
XX	PT	Polypeptide capable of forming a complex with a polypeptide comprising a	
XX	PT	baculovirus inhibitor of apoptosis repeat domain useful for treating	
XX	PT	cancer and other neoplasms.	
XX	PS	Disclosure; Fig 1A; 53pp; English.	
XX	CC	This invention relates to a substantially pure polypeptide having a	
XX	CC	length of less than 100 amino acids and capable of forming a complex with	
XX	CC	a polypeptide that includes a baculovirus inhibitor of apoptosis repeat	
XX	CC	(BIR) domain. The apoptosis pathway is known to play a critical role in	

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
CC (cIAP2) and HAPI2 (cIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC against which the peptides of the invention are targeted to bind.

XX Sequence 66 AA;

Query Match 100.0%; Score 389; DB 7; Length 66;
Best Local Similarity 100.0%; Pred. No.1.7e-39; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0;

QY 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
Db 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
61 PGCKYTL 66
61 PGCKYTL 66

RESULT 2

ADP90805

ID ADP90805 standard; peptide; 110 AA.

XX ADP90805;

DT 09-SEP-2004 (first entry)

DE Human XIAP protein BIR-3 domain.

XX protein labelling; peptide labelling;

XX irreversible affinity tagging residue;

XX pharmaceutical agent; human; XIAP; BIR-3.

XX Homo sapiens.

PN WO2004051270-A2.

PD 17-JUN-2004.

PF 04-DEC-2003; 2003WO-EP013715.

PR 05-DEC-2002; 2002GB-00028429.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

PI Auer M, Meisner N, Selfert J;

DR WPI; 2004-480677/45.

PT Providing labeled target protein or target peptide by contacting chemical
PT compound with affinity support, removing impurities in reaction mixture
PT surrounding affinity support, cleaving or eluting chemical molecule from
PT affinity support.

PS Example 6; Page 46; 81pp; English.

XX The invention comprises a method for providing a labelled target
CC protein/peptide. The method involves contacting a chemical compound with
CC affinity support, removing impurities in the reaction mixture surrounding
CC the affinity support to which the chemical molecule is bound, and
CC cleaving or eluting the molecule from the affinity support to obtain
CC irreversible or reversible affinity tagging residue, labelled target
CC protein or labelled peptide. The method of the invention is useful for
CC labelling a target protein/peptide or high throughput screening assay.
CC The method of the invention is useful for identifying agents that
CC modulate the activity or characteristics of a target protein/peptide -
CC such agents are useful as pharmaceuticals. The present amino acid
CC sequence represents the BIR-3 domain from the human XIAP protein which
CC was used in an example of the invention.

XX Sequence 110 AA;

Query Match 100.0%; Score 389; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No.3.1e-39; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0;

QY 1 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 60
Db 17 YEARIFTFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKMY 76
61 PGCKYTL 66
77 PGCKYTL 82

RESULT 3

ABG32418

ID ABG32418 standard; protein; 236 AA.

XX ABG32418;

DT 15-NOV-2002 (first entry)

DE X-linked inhibitor of apoptosis protein, XIAP.

XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;

XX fertility; testicular cancer; male infertility; male birth control;

XX X-linked inhibitor of apoptosis protein; XIAP.

XX Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note="Encoded by mm; start codon is illegible in
FT specification"

PN US2002086409-A1.

PD 04-JUL-2002.

PF 18-DEC-2001; 2001US-00024433.

PR 29-JAN-1998; 98US-0073001P.

PR 29-JAN-1999; 99US-00239867.

PA (KORN/) KORNEIUK R G.

PA (LAGA/) LAGACE M.

PI Korneiuk RG, Lagace M;

DR WPI; 2002-642245/69.

DR N-PSDB; ABS52803.

PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins
PT that is expressed in testes useful for modulating apoptosis in cells,
PT particular cells involved in male fertility.

PS Example 3; Fig 4B; 24pp; English.

XX	A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
CC	apoptosis) family of proteins that is expressed in the testes. (I) is
CC	useful for identifying a compound that modulates TIAP biological activity
CC	(I) is useful for increasing apoptosis in a cell, preferably a germ-line
CC	cell and for increasing fertility in an animal. (I) is useful for
CC	treating or preventing apoptosis which occurs as a part of testicular
CC	cancer and male infertility. TIAP may be manipulated for use as a male
CC	birth control. TIAP polypeptides and nucleic acid sequences also have
CC	diagnostic use in the detection or monitoring of conditions involving
CC	aberrant levels of apoptosis. The present sequence represents the amino
CC	acid sequence of X-linked inhibitor of apoptosis protein, XIAP
XX	
SQ	Sequence 236 AA;
Query Match	100.0%; Score 389; DB 5; Length 236;
Best Local Similarity	100.0%; Pred. No. 7,5e-39;
Matches	66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy	1 YEARIFTFGTWISYVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPMEQHAKMY 60
Db	4 YEARIFTFGTWISYVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSDDPMEQHAKMY 63
Oy	61 PGCKYL 66
Db	64 PGCKYL 69
RESULT 4	
AAO20511	AAO20511 standard; protein, 278 AA.
XX	AAO20511;
AC	
XX	27-JUN-2002 (first entry)
DT	
XX	Protein of APP related human homologue hCP5J211.
DE	
XX	Neuroprotective; nocotropic; transgenic fly; Alzheimer's disease; Abeta;
KM	amyloid precursor protein; tissue-specific expression control; human APP;
KW	APP pathway modulator; gene therapy.
XX	
OS	Homo sapiens.
XX	
XX	MO200226820-A2.
PN	
XX	04-APR-2002.
PD	
PF	01-OCT-2001; 2001WO-EP011345.
XX	
PR	29-SEP-2000; 2000US-0236893P.
XX	
PR	14-JUN-2001; 2001US-0238309P.
XX	
PA	(NOVS) NOVARTIS AG.
XX	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI	Cohen D, Dengler UT, Finelli AL, Freuler F, Konsolaki M;
PI	Reinhardt MMHM, Zuesman S;
DR	WI; 2002-315796/35.
N-PSDB; AAK99405.	
XX	
PT	New transgenic fly, containing DNA encoding an Abeta portion of human
PT	APP, useful for identifying agents which modulate the APP pathway and
XX	which can be used to treat Alzheimer's disease.
XX	
PS	Example 4; Page 112; 129pp; English.
XX	
CC	The invention relates to a transgenic fly whose genome comprises DNA
CC	encoding a polypeptide having the Abeta portion of human amyloid
CC	precursor protein (APP), fused to a signal sequence. The DNA sequence
CC	encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC	the specification. The DNA sequence is operably linked to a tissue-

Query Match	Similarity	Score	DB	Length	Best Local	Matches	Conservative	Mismatches	Indels	Gaps
1	YEARIFPGTWIVSVNKEQLARAGFYALGEGDVKCFPHCGGLTDMKPSDDPMEQHA	60								
46	YEARIFPGTWIVSVNKEQLARAGFYALGEGDVKCFPHCGGLTDMKPSDDPMEQHA	105								
61	PGCKYL	66								
106	PGCKYL	111								
RESULT 5										
AAW19581	standard; protein; 497 AA.									
02-SEP-1997	(first entry)									
Human apoptosis inhibitor XIAP.										
Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; leukaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis.										
Homo sapiens.										
Location/Qualifiers										
Key	26.93									
Domain	/label= BIR-1									
Domain	163.230									
Domain	/label= BIR-2									
Domain	265.330									
Domain	/label= BIR-3									
Domain	439.484									
Domain	/label= Ring_zinc_finger									
W09706255-A2.										
20-FEB-1997.										
05-AUG-1996; 96WO-IB001022.										
04-AUG-1995; 95US-00511485.										
22-DEC-1995; 95US-00576956.										
(UYOT-) UNIV OTTAWA.										
Korneluk RG, Mackenzie AE, Baird S, Liston P;										
WPI; 1997-154262/14.										
N-PSDB; AAT70836.										
Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease.										
Claim 27; Page 68-70; 219pp; English.										

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP) and which are characterised by the presence of a zinc
CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
CC deduced from the xiap gene (AA170836) isolated from a human foetal brain
CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
CC or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease
XX

SQ Sequence 497 AA;
Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKWY 60
DB 265 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKWY 324
61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 6
AAW69294
ID AAW69294 standard; protein; 497 AA.
XX
AC AAW69294;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human XIAP protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM proliferative disease; IAP; therapy; cancer; human; XIAP protein.
XX
OS Homo sapiens.
XX
EN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
XX WPI, 1998-467164/40.
DR N-PSDB; AAV55038.
XX
XX

Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Disclosure; Fig 1; 147pp; English.
XX
XX This sequence is the human XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX

SQ Sequence 497 AA;
Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKWY 60
DB 265 YEARIPTFGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDPMEOHAKWY 324
61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 7
AAV59451
ID AAV59451 standard; protein; 497 AA.
XX
AC AAV59451;
XX
DT 24-MAR-2000 (first entry)
XX
DE Human XIAP protein sequence.
XX
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KM transforming growth factor-beta activated kinase 1; monocyte migration;
KM TAK1 binding protein 1; extracellular matrix protein production;
KM cell growth inhibitor; beta-amyloid protein deposition;
KM immunosuppression; Transforming growth factor-beta.
XX
OS Homo sapiens.
XX
PN JP11326328-A.
XX
PD 26-NOV-1999.
XX
PF 13-MAY-1998; 98JP-00130378.
XX
PR 13-MAY-1998; 98JP-00130378.
XX
PA (MATS/) MATSUMOTO K.
XX WPI; 2000-078337/07.
DR N-PSDB; AA248662.
XX
XX

Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein.
XX
PS Claim 3; Page 28-30; 43pp; Japanese.
XX
XX This sequence represents the human XIAP protein. The invention relates to
CC a method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (Transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 8

ID AAY99985 standard; protein; 497 AA.

XX AAY99985;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis.

XX X-linked inhibitor of apoptosis; XIAP; hIAP; MHA; U45880; antisense;
 KM antiinflammatory; cytostatic; tumour.

XX Homo sapiens.

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-00392580.

XX 09-SEP-1999; 99US-00392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CP, Cowbert LM, Ackermann EJ;

XX WPI; 2000-498201/44.
 DR N-PSDB; AAA64901.

PT Antisense compound useful for research reagents, diagnostics, prophylaxis
 PT and for treating disorders associated with X-linked inhibitor of
 PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

PS Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis (the
 CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated with
 CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
 CC prophylactically to prevent infection, inflammation or tumour formation

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330

DB 325 PGCKYL 330

RESULT 9

ID ABG65663 standard; protein; 497 AA.

XX ABG65663;

XX 26-AUG-2002 (first entry)

XX Human inhibitor of apoptosis, XIAP.

XX Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
 KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
 KM embryonic development; viral pathogenesis; autoimmune disorder;
 KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
 KM herpes virus infection; pox virus infection; adenovirus infection;
 KM proliferative disease.

XX Homo sapiens.

XX W0200226968-A2.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-CA001379.

XX 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

XX N-PSDB; ABK93869.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

PS Example 12; Fig 1; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer, and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence

SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 5; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMEOHAKMY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 10

ADB80961 ID ADB80961 standard; protein; 497 AA.

AC ADB80961;

DT 04-DEC-2003 (first entry)

XX RING-SH complex related protein, SEQ ID NO 35.

XX RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hep60;

KM Hep70; Hep90; STAM1; STAM2A; STAM2B; VHS-UIW; GTPase; E2 enzyme; tsg101;

KM cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;

XX rhadovirus; filovirus.

XX Undenitified.

XX WO2003033646-A2.

XX 24-APR-2003.

XX 31-JUL-2002; 2002WO-US024589.

XX 31-JUL-2001; 2001US-0308958P.

XX 09-NOV-2001; 2001US-0345846P.

XX (PROT-) PROTEOLOGICS INC.

XX Greener T, Moskowitz H, Reiss Y, Alroy I;

XX WPI; 2003-393509/37.

XX N-PSDB; ADB81002.

XX New isolated protein complex comprising a RING-SH 3 polypeptide and

XX another polypeptide, useful for detecting cells infected with a virus,

XX and for treating viral disorders caused by retroviruses, rhadoviruses,

XX or filoviruses.

XX Disclosure; Fig 35; 176pp; English.

XX The invention relates to a novel isolated protein complex comprising a

XX RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a

XX Gag late domain, PI3K, actin, myosin, Hep60, Hep70, Hep90, STAM1, STAM2A,

XX STAM2B, VHS-UIW, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a

XX clathrin. The novel protein complex has virucide activity and can be used

XX to treat disorders as part of a vaccine. The protein complex and

XX composition are useful for detecting cells infected with a virus, for

XX identifying agents having antiviral activity, and for treating viral

XX disorders caused by retroviruses, rhadoviruses, or filoviruses. This

XX sequence is a protein comprising the RING-SH complex of the invention.

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 7; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDDPWEQHAQWY 60
 DB 265 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDDPWEQHAQWY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 11

AD139804

ID AD139804 standard; protein; 497 AA.

XX AD139804;

XX 15-APR-2004 (first entry)

XX Human inhibitor of apoptosis-like protein (IAP).

XX Inhibitor of apoptosis-like protein; IAP; IAP; apoptosis; therapy;

KM cancer; cell immortalisation; cysteine protease; viral infection;

XX cytosolic; virucide; human.

XX Homo sapiens.

XX US6511828-B1.

XX 28-JAN-2003.

XX 31-MAY-1996; 96US-00657759.

XX 31-MAY-1996; 96US-00657759.

XX (ARCH-) ARCH DEV CORP.

XX Thompson CB, Duckett CS;

XX WPI; 2003-391256/37.

XX New inhibitor of apoptosis-like protein (IAP) and polynucleotide encoding

XX IAP, useful for inhibiting or stimulating apoptosis in target cells,

XX treating certain cancers, or sustaining host cell survival following

XX viral infection.

XX Claim 1; SEQ ID NO 2; 42pp; English.

XX The present invention relates to inhibitor of apoptosis (IAP)-like

XX proteins (IAP) and polynucleotides encoding such proteins. Sequences of

XX the invention are useful for inhibiting or stimulating apoptosis in

XX target cells or for treating certain cancers. They are also useful in the

XX immortalisation of cells for culture, for inhibiting the activation of

XX cysteine proteases and to sustain host cell survival following viral

XX infection. The IAP may also be used as a marker in gel separation

XX procedures or as a standard in protein concentration determinations. The

XX present sequence is human inhibitor of apoptosis-like protein.

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 7; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.8e-38;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDDPWEQHAQWY 60

DB 265 YEARITFTGWTIVSVNKEQLARAGFYALGEGDKVCKFHCGGGLTDMKPSDDPWEQHAQWY 324

QY 61 PGCKYL 66
 DB 325 PGCKYL 330

RESULT 12

ADH74639

ID ADH74639 standard; protein; 497 AA.

XX ADH74639;

XX 15-APR-2004 (first entry)

XX Human XIAP polypeptide.

XX Biomarker; prostate neoplastic condition; inhibitor of apoptosis; IAP;

XX XIAP; X chromosome-linked inhibitor of apoptosis; CIAP1, CIAP2;

XX prostate cancer; human.

XX Homo sapiens.
 OS US2003224399-A1.
 PN XX
 XX 04-DEC-2003.
 PD
 XX 12-FEB-2003; 2003US-00366307.
 PF
 XX 12-FEB-2002; 2002US-0356956P.
 PR
 XX (REED/) REED J C.
 PA (KRAU/) KRAJEWSKI S.
 XX
 PI Reed JC, Krajewski S;
 XX
 XX WPI; 2004-141816/14.
 DR N-PSDB; ADH74638.
 XX
 PT Identifying biomarker that is diagnostic for survival of a patient with
 PT prostate neoplastic condition by measuring level of integrin associated
 PT protein in sample, and identifying correlation of the level in sample.
 PS
 PS Disclosure; SEQ ID NO 2; 42bp; English.
 XX
 CC The present invention relates to a method for identifying a biomarker
 CC that is diagnostic for the survival of patient with a prostate neoplastic
 CC condition. The method comprises measuring the level of inhibitor of
 CC apoptosis (IAP) polypeptide chosen from chosen from XIAP (X chromosome-
 CC linked inhibitor of apoptosis), CIAP1 and CIAP2 in a neoplastic prostate
 CC cell-containing sample from patients, and identifying correlation between
 CC the level of IAPs in the sample, where the correlation of an IAP with
 CC survival in the patients indicates IAP as a biomarker diagnostic. The
 CC method is useful for the prognosis of prostate neoplastic conditions such
 CC as prostate cancer. The method is efficient in determining the prognosis
 CC while the patient is still at an early stage of disease, and in
 CC monitoring the effectiveness of a particular treatment in a prostate
 CC neoplastic condition. The present sequence represents human XIAP.
 CC
 SQ Sequence 497 AA;
 Query Match 100.0%; Score 389; DB 8; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGSDVKYKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGSDVKYKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 13
 ID ADL70166 standard; protein; 497 AA.
 AC ADL70166;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human X chromosome linked inhibitor of apoptosis (XIAP).
 XX
 KM Human; inhibitor of apoptosis; IAP; XIAP; Hodgkin's disease; cytostatic;
 KM gene therapy; gene silencing.
 OS Homo sapiens.
 XX
 PN WO2004017991-A1.
 XX
 PD 04-MAR-2004.
 XX

PF 18-JUL-2003; 2003WO-EP007889.
 XX
 PR 13-AUG-2002; 2002DE-01037139.
 XX
 PA (CELL-) CELL CENT COLOGNE GMBH.
 XX
 PI Kroenke M, Kaehkar H, Hamilton-Dutoit SJ, Juergensmeier JM;
 XX
 XX WPI; 2004-226745/21.
 DR N-PSDB; ADL70165.
 XX
 PT Using inhibitors of apoptosis-inhibitor for preparation of pharmaceutical
 PT composition for treatment of Hodgkin's lymphomas.
 PS
 PS Claim 11; SEQ ID NO 2; 61bp; English.
 XX
 CC The present sequence is the protein sequence of human X chromosome linked
 CC inhibitor of apoptosis (XIAP). The invention is based on the discovery
 CC that IAPs, e.g. XIAP, are constitutively overexpressed in both Hodgkin's
 CC lymphoma (HL)-derived B-cell lines and in primary HL tissues, and that in
 CC B-cell lines they are associated with and inhibit in particular caspase-
 CC 3. Based on this finding, the invention provides a new therapy of HL,
 CC which is based on inhibitors of IAPs, especially XIAP, that reduce or
 CC eliminate the caspase inhibiting activity. The approach leads to the
 CC restoration of apoptotic mechanisms, which result in an increased number
 CC of cell death events in malignant HL cells. Since IAPs, in particular
 CC XIAP, are not overexpressed in normal tissues, the approach provides a
 CC selective therapy for HL. Suitable IAP inhibitors include molecules that
 CC reduce the level of IAP mRNA, reduce the level of the IAP, inhibit the
 CC binding of the IAP to a caspase or reduce the biological activity of the
 CC IAP, e.g. an antisense nucleic acid, short interfering RNA (siRNA),
 CC ribozyme, anti-IAP antibody, anti-IAP aptamer, small molecule, peptide or
 CC peptidomimetic. Diagnostic methods for the detection of HL using IAP
 CC specific agents are also provided.
 CC
 SQ Sequence 497 AA;
 Query Match 100.0%; Score 389; DB 8; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIPTFGTWISVNKEQLARAGFYALGSDVKYKCFHCGGGLTDMKPSDPMEOHAKMY 60
 DB 265 YEARIPTFGTWISVNKEQLARAGFYALGSDVKYKCFHCGGGLTDMKPSDPMEOHAKMY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 RESULT 14
 ID ADP23982 standard; protein; 497 AA.
 AC ADP23982;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO:1160.
 XX
 KM PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX

XX (GENTH) GENENTECH INC.
 XX PA
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI,
 PI Wu TD;
 XX WPI: 2004-419628/39.
 DR N-PSDB; ADP23981.
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythemaecus, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 XX Claim 7, SEQ ID NO 1160; 2940pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipruritic, antiallergic,
 CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 CC
 XX
 XX Sequence 497 AA;
 SQ
 Query Match 100.0%; Score 389; DB 8; Length 497;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEARIFFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAQWY 60
 DB 265 YEARIFFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAQWY 324
 QY 61 PGCKYL 66
 DB 325 PGCKYL 330
 DB ADB61827 standard; protein; 66 AA.
 ID ADB61827
 XX
 XX ADB61827;
 AC
 XX
 DT 04-DEC-2003 (first entry)
 XX
 XX Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
 XX
 XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;

KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilms' tumour; BIR 3 domain; rat.
 XX
 XX Rattus sp.
 XX
 XX WO2003040172-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 12-NOV-2002; 2002WO-CA001738.
 XX
 XX 09-NOV-2001; 2001US-033230P.
 XX
 XX 08-APR-2002; 2002US-0370934P.
 XX
 XX (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Boudreaux A, Korneluk RG, La Casse E, Lister P;
 PI WPI: 2003-513532/48.
 XX
 XX
 PT Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 XX Disclosure; Fig 1B; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
 CC which was used to demonstrate homology to human IAP protein BIR domains
 CC to which the peptides of the invention are targeted to bind.
 CC
 XX
 XX Sequence 66 AA;
 SQ
 Query Match 96.9%; Score 377; DB 7; Length 66;
 Best Local Similarity 95.5%; Pred. No. 5e-38;
 Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YEARIFFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAQWY 60
 DB 1 YDARIIVTFTGWTWYSVNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDDPWEQHAQWY 60
 QY 61 PGCKYL 66
 DB 61 PGCKYL 66
 DB AAM19745 standard; protein; 496 AA.
 ID AAM19745
 XX
 XX AAM19745
 XX
 XX AAM19745 standard; protein; 496 AA.

```

XX AC AAW19745;
XX DT 16-SEP-1997 (first entry)
XX DE Mouse inhibitor of apoptosis protein homologue MIHA.
XX KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX KM degenerative disease; infectious disease; autoimmune disease; cancer;
XX KW therapy; diagnosis.
XX OS Mus musculus.
XX FH Key
XX FT Region
XX FT Region
XX FT Region
XX FT Region
XX FT Region
XX FT Region
XX FT Region
XX PN W09723501-A1.
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU000827.
XX PR 22-DEC-1995; 95AU-00007275.
XX PR (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PA
XX PI Vaux DL;
XX DR WPI; 1997-350966/32.
XX DR N-PSDB; AAT72710.
XX PT Isolated protein homologues of viral inhibitors of apoptosis - used to
XX PT modulate apoptosis for treatment of degenerative, infectious or
XX PT auto-immune diseases and cancer.
XX PS Claim 7; Page 44-47; 136pp; English.
XX CC Mammalian IAP homologue A (MIHA) (AAW19745) is a murine homologue of
XX CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence
XX CC was deduced from a cDNA clone (see also AAT72710) isolated from a mouse
XX CC liver cDNA library on the basis of homology to Oryzias pseudotsugata
XX CC polyhedrosis virus IAP BIR and RING finger amino acid motifs (see also
XX CC AAW19744). IAP homologues (see also AAW19746-52) and their derivatives
XX CC and chemical analogues can be used in methods for modulating apoptosis in
XX CC animal cells, specifically for treatment, by inhibition, of degenerative
XX CC and infectious disease or, by promotion, of cancer and autoimmune disease
XX SQ Sequence 496 AA;

Query Match 94.6%; Score 368; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 6.3e-36;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDMKPSBDPMEQIAKMY 60
Db 264 YEARIIVFGTWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDMKPSBDPMEQIAKMY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 17
AAW19584
ID AAW19584 standard; protein; 496 AA.
XX

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AC AAW19584;
XX DT 02-SEP-1997 (first entry)
XX DE Mouse apoptosis inhibitor M-XIAP.
XX KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
XX KM HIV; AIDS; neurodegeneration; myelodysplastic syndrome; leukaemia;
XX KM myocardial infarction; stroke; reperfusion injury;
XX KW toxin-induced liver disease; gene therapy; diagnosis.
XX OS Mus sp.
XX FH Key
XX FT Domain
XX FT Domain
XX FT Domain
XX FT Domain
XX FT Domain
XX FT Domain
XX FT Domain
XX PN W09706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB001022.
XX PR 04-AUG-1995; 95US-00511485.
XX PR 22-DEC-1995; 95US-00576956.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Korneljuk RG, Mackenzie AB, Baird S, Liston P;
XX DR WPI; 1997-154262/14.
XX DR N-PSDB; AAT70839.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
XX PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
XX PT susceptibility to apoptotic disease.
XX PS Claim 27; Page 79-80; 219pp; English.
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
XX CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
XX CC of apoptosis (IAP) and which are characterised by the presence of a ring
XX CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
XX CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
XX CC was deduced from the m-xiap gene (AAT70839) isolated from a mouse embryo
XX CC cDNA library. The IAP oligopeptides can be expressed in host cells (in
XX CC vitro or in vivo) and used in methods for treating diseases and disorders
XX CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
XX CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
XX CC an ischaemic injury, selected from myocardial infarction, stroke,
XX CC reperfusion injury, or a toxin-induced liver disease
XX SQ Sequence 496 AA;

Query Match 94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 1.1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDMKPSBDPMEQIAKMY 60
Db 264 YEARIIVFGTWTIVSVNKEQLARAGFYALGEGDKVCFHGGGLTDMKPSBDPMEQIAKMY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

```

RESULT 18
AAW6297
ID AAW6297 standard; protein; 496 AA.
XX
AC AAW6297;
XX
DT 13-NOV-1998 (first entry)
XX
DE Murine XIAP protein.
XX
KM Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX
OS Mus sp.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneljuk R, Mackenzie AE, Iliston P, Baird S, Tsang B, Pratt C;
XX
XX WPI; 1998-467164/40.
DR N-PSDB; AAV55041.
XX
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Disclosure; Fig 4; 147p; English.
XX
XX This sequence is the murine XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver, nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors
SQ Sequence 496 AA;

Query Match 94.1%; Score 366; DB 2; Length 496;
Best Local Similarity 95.5%; Pred. No. 1,1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 60
DB 264 YEARIPTFGTWISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 19
ABG65666
ID ABG65666 standard; protein; 496 AA.
XX
AC ABG65666;
XX

DT 26-AUG-2002 (first entry)
XX
XX Mouse inhibitor of apoptosis, XIAP.
XX
XX Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KM cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KM embryonic development; viral pathogenesis; autoimmune disorder;
KM neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KM herpes virus infection; pox virus infection; adenovirus infection;
KM proliferative disease.
XX
XX
OS Mus sp.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CM001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PA (ABGR-) ABERRA THERAPEUTICS INC.
XX
PI Korneljuk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
XX WPI; 2002-479562/51.
DR N-PSDB; ABK93872.
XX
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 4; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
XX nucleic acid (I) that inhibits IAP biological activity, regardless of
XX length of the antisense nucleic acid, the IAP proteins may be mouse or
XX human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
XX composition comprising a mammalian IAP antisense molecule and a method of
XX enhancing apoptosis in a cell, comprising administering a negative
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX mammal diagnosed with a proliferative disease. The method is useful for
XX treating a patient diagnosed with a proliferative disease like cancer.
XX The IAP antisense molecule is useful to treat, ameliorate, improve,
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or
XX conditions where apoptosis is involved or implicated (e.g. embryonic
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX virus, pox virus and adenovirus). The present sequence is a mouse IAP
XX protein sequence
SQ Sequence 496 AA;

Query Match 94.1%; Score 366; DB 5; Length 496;
Best Local Similarity 95.5%; Pred. No. 1,1e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 60
DB 264 YEARIPTFGTWISVVKQOLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPMEQHAKY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 20
ADB61828
ID ADB61828 standard; protein; 66 AA.
XX

AC	AD861828;	
XX		
DT	04-DEC-2003	(first entry)
XX		
DE	Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.	
XX		
KM	baculovirus inhibitor of apoptosis repeat domain; BIR domain;	
KM	apoptosis pathway; embryonic development; viral pathogenesis; cancer;	
KM	autoimmune disorder; neurodegenerative disease; apoptotic response;	
KM	systemic lupus erythematosus; multiple sclerosis; viral infection;	
KM	herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;	
KM	HIAP1; cIAP2; HIAP2; cIAP1; RING zinc finger; caspase-3; caspase-7;	
KM	caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;	
KM	cervical cancer; uterine cancer; testicular cancer;	
KM	small cell lung carcinoma; uterine cancer; renal cell carcinoma;	
KM	Wilm's tumour; BIR 3 domain; mouse; murine.	
XX		
OS	Mus sp.	
XX		
PN	WO2003040172-A2.	
XX		
PD	15-MAY-2003.	
XX		
PF	12-NOV-2002; 2002MO-CA001738.	
XX		
PR	09-NOV-2001; 2001US-032300P.	
PR	08-APR-2002; 2002US-0370934P.	
XX		
PA	(AEGE-) AEGERA THERAPEUTICS INC.	
XX		
PI	Boudreault A, Korneluk RG, La Casse E, Liston P;	
XX		
DR	WPI; 2003-513532/48.	
XX		
PT	Polypeptide capable of forming a complex with a polypeptide comprising a	
PT	baculovirus inhibitor of apoptosis repeat domain useful for treating	
XX	cancer and other neoplasms.	
XX		
PS	Disclosure; Fig 1B; 53pp: English.	
XX		
CC	This invention relates to a substantially pure polypeptide having a	
CC	length of less than 100 amino acids and capable of forming a complex with	
CC	a polypeptide that includes a baculovirus inhibitor of apoptosis repeat	
CC	(BIR) domain. The apoptosis pathway is known to play a critical role in	
CC	embryonic development, viral pathogenesis, cancer, autoimmune disorders	
CC	and neurodegenerative diseases. The failure of the apoptotic response has	
CC	been implicated in the development of cancer, autoimmune disorders (for	
CC	example systemic lupus erythematosus and multiple sclerosis) and viral	
CC	infections (including herpes virus, poxvirus and adenovirus. The	
CC	inhibitors of apoptosis (IAPs) are a family of proteins possessing one or	
CC	more baculovirus IAP repeat (BIR) domain. Human IAPs, XIAP, HIAP1	
CC	(cIAP2) and HIAP2 (cIAP1) all possess three BIR domains and carboxy	
CC	terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and	
CC	-9 which are proteases involved in the initiation of apoptosis. Compounds	
CC	which inhibit the activity of IAPs may therefore have cytostatic activity	
CC	through the enhancement of apoptosis. The polypeptides of the invention	
CC	are candidate peptide ligands for binding to the BIR domain of IAPs. They	
CC	may be useful for the treatment of cancer and other neoplasms, such as	
CC	leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular	
CC	cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma	
CC	and Wilm's tumour, and for enhancing apoptosis. The present sequence is	
CC	that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain	
CC	which was used to demonstrate homology to human IAP protein BIR domains	
CC	to which the peptides of the invention are targeted to bind.	

Query Match	90.5%	Score 352	DB 7	Length 66
Best Local Similarity	92.4%	Pred. No. 5	5e-35	
Matches 61	Conservative 1	Mismatches 4	Indels 0	Gaps 0
QY	1	YEAR1FTGCTW1SYNKEQLADAGFYALGEGKVKCFHGGSLTDMKPSDEDMEQHAKKY	60	

Db 1 YEARIIVTFGWITSSVKNKEQLARAGFTALGEGDNYKCFHCGGGLTDWKPSSEDPMDQIAKCY 60

QY 61 PGCKYL 66
|||

Db 61 PGCKYL 66

RESULT 21	
ABP72157	
ID	ABP72157 standard; protein; 496 AA.
XX	
AC	ABP72157;
XX	
DT	22-APR-2003 (first entry)
XX	
DE	Mouse inhibitor of apoptosis protein MIAP3.

KW Inhibitor of apoptosis; MAP3; mouse; apoptosis; cancer; leukaemia;
 XX lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
 XX
 OS Mus sp.
 XX
 PN W02003004606-A2.
 XX
 PD 16-JAN-2003.
 XX
 XX
 PF 03-JUL-2002; 2002WO-US021002.
 XX
 XX
 PR 03-JUL-2001; 2001US-00898158.
 XX

PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX
PI Troy CM, Shelanski ML,
XX
XX WPI, 2003-210351/20.
DR N-PSDB; ABZ58102.
XX
XX
XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
PT treating cancer; neurodegenerative disorder or cardiomyopathy.
XX
XX
PS Disclosure; Fig 15A; 124p; English.

CC The present sequence is the protein sequence of murine inhibitor of
 CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as
 CC an antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2
 CC MIAP3, CIAPI, CIAI2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)
 CC
 CC Sequence 496 AA:

```

Query Match      90.5%; Score 352; DB 6; Length 496;
Best Local Similarity 92.4%; Pred. 0.56e-34;
Matches 61; Conservative 1; Mismatches 4; Indels 0; Gaps
Oy 1 YEARIETFGTWIYSVNKEQLARAGPYALBEGDVKYCFHCGGITLDMKPSBDEPWEQHAHMY 60
db 264 YEARIYVFGMTSIVNKEQLARAGPYALBEGDVKYCFHCGGITLDMKPSBDEPWEQHAHMY 322

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Oy	61	PGCXYL	66
Db	324	PGCXYL	329


```

XX SQ Sequence 236 AA;
Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 9.7e-34;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIPTFGTWIVSVNKEQLARAGFYALGSDGVKVCFCGCGGLTDMKPSDPEQHAHMY 60
Db 4 YEARIITFGTWIVSVNKEQLARAGFYALGSDGVKVCFCGCGGLANMKPKEDPMEQHAHMY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 24
AAE00365
ID AAE00365 standard; protein, 236 AA.
AC AAE00365;
DT 19-JUN-2001 (first entry)
DE Human IAP-1like protein-2 (ILP-2) with TGFbetar modulating activity.
XX
XX Human; inhibitor of apoptosis; IAP-1like protein-2; ILP-2;
XX chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
XX TGFbetar; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
XX cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
XX T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
XX retinal degeneration; hyperferritinemia-cataract syndrome; cancer;
XX autoimmune disease; diabetes; multiple sclerosis; cytosstatic.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Domain 7..70
XX /label= BIR domain
XX /note= "Baculovirus iap repeat"
XX Domain 188..223
XX /label= RING_finger_domain

WO200123568-A2.
05-APR-2001.
29-SEP-2000; 2000WO-US026735.
30-SEP-1999; 99US-0157169P.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Duckett C, Mir SS;
XX
XX WPI; 2001-258135/26.
DR N-PSDB; AAD03581.
XX
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
XX transforming growth factor beta receptor modulating activity, and the
XX PT nucleic acids that encode them, useful for treating, e.g. diabetes and
XX PT multiple sclerosis.
XX
XX Claim 1; Fig 2; 108pp; English.
XX
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
XX (ILP-2). The hILP-2 gene is located on chromosome 19q13.3-q13.4. ILP-2
XX comprises a single amino-terminal domain known as baculovirus iap repeat
XX (BIR), followed by a spacer region and a carboxy-terminal ring finger
XX domain. It interacts with transforming growth factor beta receptor
XX (TGFbetar) and modulates TGFbetar activity. It also potentially inhibits
XX apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It
XX also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in

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CC the area of genetic testing for predisposition to diseases, such as cone-
CC rod retinal dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell
CC acute lymphoblastic leukaemia, colorectal cancer and hyperferritinemia-
CC cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also
CC used in the treatment of diseases associated with abnormal apoptosis such
CC as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
CC neurodegenerative diseases including retinal degeneration. The ILP-2 gene
CC is also used in gene therapy for treating patients suffering from ILP-2
CC gene deletions or mutations
XX
XX Sequence 236 AA;
Query Match 89.2%; Score 347; DB 4; Length 236;
Best Local Similarity 84.8%; Pred. No. 9.7e-34;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIPTFGTWIVSVNKEQLARAGFYALGSDGVKVCFCGCGGLTDMKPSDPEQHAHMY 60
Db 4 YEARIITFGTWIVSVNKEQLARAGFYALGSDGVKVCFCGCGGLANMKPKEDPMEQHAHMY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 25
AAU75066
ID AAU75066 standard; protein, 236 AA.
XX
XX AAU75066;
AC
XX 23-APR-2002 (first entry)
DE Human testes specific inhibitor of apoptosis (TIAP) protein.
XX
XX TIAP; apoptosis; testes specific inhibitor of apoptosis; human;
XX apoptotic; cytostatic; anti-infertility; contraceptive;
XX chromosome 12q22-23; transgenic animal; antibody; immunogen;
XX testicular cell; testicular cancer; cancer; male infertility;
XX male birth control; XIAP.
XX
XX Homo sapiens.
OS
XX
XX US6331412-B1.
XX
XX 18-DEC-2001.
XX
XX 29-JAN-1999; 99US-00239867.
XX
XX 29-JAN-1998; 98US-0073001P.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Korneluk RG, Lagace M;
XX
XX WPI; 2002-105275/14.
DR N-PSDB; ABK13197.
XX
XX Nucleic acids encoding a testis specific apoptosis inhibitor protein
XX (TIAP) useful for treating testicular cancers, cancers in non-testicular
XX PT tissues, male infertility, and for achieving male birth control.
XX
XX Example 4; Fig 4B; 29pp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a TIAP polypeptide (testes-specific inhibitor of apoptosis) protein. This
XX gene is a homologue of the X-linked XIAP gene and is located on
XX chromosome 12q22-23. The nucleotide and protein sequences of the
XX invention and vectors containing these sequences may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate TIAP expression. Additionally, the nucleotide sequence may
XX be used to express the TIAP protein by recombinant methods. Conversely,
XX antisense nucleic acid molecules may be administered to down-regulate

```

CC TIAP expression. The nucleotide sequence, may also be used to design DNA
 CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
 CC detect and quantitate the presence of similar nucleic acid sequences in
 CC samples, to identify patients who may be in need of restorative therapy.
 CC Through the production of transgenic animals and cells, the sequences may
 CC also be used to study the expression and function of TIAP proteins and
 CC their role in metabolism. The TIAP polypeptides may be used to produce
 CC antibodies against TIAP and maybe used to identify modulators (agonists
 CC or antagonists) of TIAP expression and activity. An anti-TIAP antibody
 CC or antagonist may also be used to down-regulate TIAP expression and
 CC activity. The reagents may be used in this way for the treatment of
 CC excessive or insufficient apoptosis, particularly in testicular cells. In
 CC particular they are useful in diagnosing and treating testicular cancers,
 CC cancers in non-testicular tissues, male infertility, and for achieving
 CC male birth control. The present sequence represents the human TIAP
 CC protein sequence of the invention

XX Sequence 236 AA;

Query Match 89.2%; Score 347; DB 5; Length 236;

Best Local Similarity 84.8%; Pred. No. 9,7e-34; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIITFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQIAKMY 60

DB 4 YEARIITFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLANWKPKEDPWEQIAKMY 63

QY 61 PGCKYTL 66

DB 64 PGCKYTL 69

RESULT 26

ABG32417 standard; protein; 236 AA.

AC ABG32417;

DT 15-NOV-2002 (first entry)

DE Inhibitor of apoptosis protein, TIAP.

XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;

KW fertility; testicular cancer; male infertility; male birth control.

XX Mammalia.

OS Key Location/Qualifiers

FT Misc-difference 1 /note= "Encoded by nnn; start codon is illegible in
 FT specification"

PN US2002086409-A1.

PD 04-JUL-2002.

PF 18-DEC-2001; 2001US-00024433.

PR 29-JAN-1998; 98US-0073001P.

PR 29-JAN-1999; 99US-00239867.

XX (KORN/) KORNELUK R G.

PA (LAGA/) LAGACE M.

PI Korneeluk RG, Lagace M;

DR WPI; 2002-642245/69.

DR N-PSDB; ABS52802.

XX Novel polypeptide, a member of inhibitor of apoptosis family of proteins
 PT that is expressed in testes useful for modulating apoptosis in cells,
 PT particular cells involved in male fertility.

PS Example 3; Fig 4B; 24pp; English.

XX A substantially pure TIAP polypeptide (1), a member of IAP (inhibitor of
 CC apoptosis) family of proteins that is expressed in the testes. (1) is
 CC useful for identifying a compound that modulates TIAP biological activity
 CC (1) is useful for increasing apoptosis in a cell, preferably a germ-line
 CC cell and for increasing fertility in an animal. (1) is useful for
 CC treating or preventing apoptosis which occurs as a part of testicular
 CC cancer and male infertility. TIAP may be manipulated for use as a male
 CC birth control. TIAP polypeptides and nucleic acid sequences also have
 CC diagnostic use in the detection or monitoring of conditions involving
 CC aberrant levels of apoptosis. The present sequence represents the amino
 CC acid sequence of TIAP

XX Sequence 236 AA;

Query Match 89.2%; Score 347; DB 5; Length 236;

Best Local Similarity 84.8%; Pred. No. 9,7e-34; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIITFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQIAKMY 60

DB 4 YEARIITFGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLANWKPKEDPWEQIAKMY 63

QY 61 PGCKYTL 66

DB 64 PGCKYTL 69

RESULT 27

AAU75747 standard; protein; 464 AA.

AC AAU75747;

DT 08-MAY-2002 (first entry)

DE Human Inhibitor of apoptosis protein 7 (IAPL7) protein.

XX Human; inhibitor of apoptosis 7; IAPL7; cytostatic; antiapoptotic; IAP;

KW apoptosis; V-Rel; cancer; NF-kappaB; chromosome 19; vaccine;

KW gene therapy; hyperproliferative disease; transgenic animal; antibody.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Region 1..133 /note= "This sequence is specifically claimed in claim 1
 FT of the specification and is encoded by the nucleic acid
 FT represented in ABK14678"

PN WO200210381-A1.

PD 07-FEB-2002.

PF 18-JUL-2001; 2001WO-EP008287.

PR 28-JUL-2000; 2000EP-00116452.

XX (MERE) MERCK PATENT GMBH.

PA Hentsch B;

PI WPI; 2002-188741/24.

DR P-PSDB; ABK14677.

XX New inhibitor of apoptosis proteins and polynucleotides useful in
 PT vaccines for inducing an immune response against hyperproliferative
 PT diseases e.g. cancer.

PS Claim 1; Page 35-36; 41pp; English.

XX This invention relates to the nucleic acid and protein sequences of a

CC novel inhibitor apoptosis protein (IAP17) polypeptide. These sequences
 CC have homology to the IAP (inhibitors of apoptosis) gene family which are
 CC thought to inhibit protein kinases by regulating the anti-apoptotic activity of
 CC the V-Rel and NF-kappaB family of transcription factors. The gene for
 CC IAP17 is located on human chromosome 19. The nucleic acids of the
 CC invention are useful for screening to identify compounds that stimulate
 CC or inhibit the function or level of IAP17, where the identified compounds
 CC are useful for treating hyper-proliferative diseases such as cancer. The
 CC protein sequences may also be used to identify membrane bound or soluble
 CC receptors of IAP17 by standard receptor binding techniques. Nucleic acids
 CC encoding IAP17, may be used as hybridisation probes for cDNA and genomic
 CC DNA, or as primers for nucleic acid amplification reaction and the
 CC primers and probes may also be used to isolate full-length cDNAs and
 CC genomic clones encoding IAP17. The nucleic acid sequences are useful as
 CC diagnostic reagents for diagnosing a disease or a susceptibility to a
 CC disease by detecting mutations in the associated gene. The nucleic acid
 CC sequence is useful for chromosome localisation and tissue expression
 CC studies and is also useful for producing transgenic animals. The IAP17
 CC protein sequence may also be used to generate an anti-IAP17 antibody
 CC which is useful in screening methods for detecting the effect of added
 CC compounds on the production of mRNA and protein in cells. The sequences
 CC of the invention are also useful as vaccines for inducing an
 CC immunological response in a mammal. The present sequence represents the
 CC human inhibitor of apoptosis 7 (IAP7) protein of the invention
 CC
 SQ Sequence 464 AA;

Query Match 89.2%; Score 347; DB 5; Length 464;
 Best Local Similarity 84.8%; Pred. No. 2.1e-33;
 Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 60
 DB 232 YEARLITFGTMYVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 291

QY 61 PGCKYL 66
 DB 292 PGCKYL 297

RESULT 28

ADR44576 ADR44576 standard; protein; 87 AA.

AC ADR44576;

DT 18-NOV-2004 (first entry)

DE X-IAP BIR3 domain.

XX BIR domain binding oligopeptide; BDR oligopeptide;
 XX melanoma inhibitor of apoptosis; ML-IAP; caspase inhibition; apoptosis;
 XX cancer; IAP antagonist; baculovirus IAP repeat domain; BIR domain;
 XX melanoma; breast cancer; colorectal cancer; lung cancer; ovarian cancer;
 XX central nervous system cancer; liver cancer; bladder cancer;
 XX pancreatic cancer; cervical cancer; leukaemia; fruit fly; sickle;
 XX small subunit; N-terminal; X-IAP.

OS Unidentified.

PN US2004171554-A1.

PD 02-SEP-2004.

PF 07-FEB-2003; 2003US-00364645.

PR 07-FEB-2003; 2003US-00364645.

PA (GERTH) GENENTECH INC.

PI Debnayes K, Fairbrother W, Flygare J, Franklin MC, Fischer S,
 PI Vucic D;

DR WPI; 2004-651687/63.

XX New isolated BIR domain binding (BDR) oligopeptide that specifically
 PT binds melanoma inhibitor of apoptosis (ML-IAP) and releases the
 PT inhibitory effect that ML-IAP has on caspase activity, useful for
 PT increasing apoptosis in cells.

XX Example 10; Fig 5; 50pp; English.

XX The invention describes an isolated BIR domain binding (BDR) oligopeptide
 CC that specifically binds melanoma inhibitor of apoptosis (ML-IAP) and
 CC releases the inhibitory effect that ML-IAP has on caspase activity. Also
 CC described are: a method of increasing apoptosis in a cell comprising
 CC contacting the cell with the oligopeptide, where the apoptosis is
 CC increased; an article of manufacture comprising a container; the
 CC composition of matter contained within the container; and a label affixed
 CC to the container, or a package insert included with the container,
 CC referring to the use of the composition of matter for the therapeutic
 CC treatment of or the diagnostic detection of a cancer; a method of
 CC screening antagonists of IAP polypeptides comprising co-crystallising the
 CC potential antagonist with the Baculovirus IAP repeat (BIR) domain of an
 CC ML-IAP polypeptide to form a co-crystalline structure and determining if
 CC the potential antagonist binds to the BIR domain; determining whether the
 CC antagonist increases apoptosis in cells relative to antagonist untreated
 CC cells; a method of screening antagonists of an ML-IAP polypeptide
 CC comprising co-crystallising the potential antagonist with the BIR domain
 CC of an ML-IAP polypeptide to form a co-crystalline structure and
 CC determining if the potential antagonist binds to the BIR domain, and
 CC where binding occurs if there is at least one contact between a specific
 CC amino acid residue of a given patch and the candidate molecule that is
 CC less than or equal to 2.8 angstroms in the co-crystalline structure. The
 CC oligopeptide and composition of matter are useful for increasing
 CC apoptosis in cells, preferably cancer cells such as a melanoma cell, a
 CC breast cancer cell, a colorectal cancer cell, a lung cancer cell, an
 CC ovarian cancer cell, a central nervous system cancer cell, a liver cancer
 CC cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer
 CC cell, and a leukaemia cell. This is the amino acid sequence of IAP BIR
 CC domain associated with the selection of BIR domain binding oligopeptides.
 CC
 SQ Sequence 87 AA;

Query Match 88.0%; Score 342.5; DB 8; Length 87;
 Best Local Similarity 90.9%; Pred. No. 1.1e-33;
 Matches 60; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 YEARIFPGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 60
 DB 9 YEARXXTFGTWIVSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDPMWEOHAKMY 67

QY 61 PGCKYL 66
 DB 68 PGCKYL 73

RESULT 29

AAE00366 AAE00366 standard; protein; 236 AA.

AC AAE00366;

DT 19-JUN-2001 (first entry)

DE Chimpanzee IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.

XX Chimpanzee; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
 XX transforming growth factor beta receptor; TGFbetaR;
 XX c-Jun N-terminal kinase; JNK; gene therapy; glucaricaciduria;
 XX cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
 XX T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
 XX retinal degeneration; hyperferritinemia-cataract syndrome; cancer;
 XX autoimmune disease; diabetes; multiple sclerosis; cytostatic.
 OS Pan troglodytes.

Gorilla IAP-like protein-2 (ILP-2) with TGFbeta modulating activity.

Gorilla; Inhibitor of apoptosis; IAP-like protein-2; ILP-2; transforming growth factor beta receptor; TGFbeta; cytoskeletal; c-Jun N-terminal kinase; JNK; gene therapy; glaucomatous retinopathy; acute lymphoblastic leukaemia; neurodegenerative disease; retinal degeneration; hyperferritinemia-cataract syndrome; cancer; autoimmune disease; diabetes; multiple sclerosis.

Gorilla gorilla.
WO200123568-A2.
05-APR-2001.
29-SEP-2000; 2000MO-US026735.
30-SEP-1999; 99US-0157169P.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Duckett C, Mir SS;
WPI; 2001-258135/26.
N-PDB; AAD03583.

Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with transforming growth factor beta receptor modulating activity, and the nucleic acids that encode them, useful for treating, e.g. diabetes and multiple sclerosis.

Claim 1; Fig 2; 108pp; English.

The present sequence is gorilla inhibitor of apoptosis (IAP)-like protein -2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain known as baculovirus iap repeat (BIR), followed by a spacer region and a carboxy-terminal ring finger domain. It interacts with transforming growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in the area of genetic testing for predisposition to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa, glaucosarcoma, T-cell acute lymphoblastic leukemia, colorectal cancer and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also used in the treatment of diseases associated with abnormal apoptosis such as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and neurodegenerative diseases including retinal degeneration. The ILP-2 gene is also used in gene therapy for treating patients suffering from ILP-2 gene deletions or mutations

Sequence 236 AA;

Query Match 86.9%; Score 338; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 1,2e-32;
Matches 54; Conservative 7; Mismatches 5; Indels 0; Gaps 0

OY 1 YEARIFTGTYISVYNKQOLARAGFYALAGEGNKVCFCFGGLTMKRSEDEPWCHAKMY 60
Db ||||| :||||| :||||| :||||| :|||||
ID 4 YEAMLTITGTWMYSVNKEQLARAGFYAIGQEDKIQCFCFGGLTAWKPKEDPEWHOKAMY 63
OY 61 PGCKYL 66
Db 64 FGCKYL 69

RESULT 32
ADB61832
ID ADB61832 standard; protein; 57 AA.
AC ADB61832;
XX

DT	04-DEC-2003	(first entry)	
XX	Unidentified inhibitor of apoptosis (IAP) protein IAP BIR3 domain.		
DE			
XX			
XX	baculovirus inhibitor of apoptosis repeat domain; BIR domain;		
KW	apoptosis pathway; embryonic development; viral pathogenesis; cancer;		
KW	autoimmune disorder; neurodegenerative disease; apoptotic response;		
KW	systemic lupus erythematosus; multiple sclerosis; viral infection;		
KW	herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;		
KW	HIAP1; CIAP2; XIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;		
KW	caspase-9; cytosolic; neoplasm; leukaemia; colon carcinoma;		
KW	cervical cancer; uterine cancer; testicular cancer;		
KW	small cell lung carcinoma; uterine cancer; renal cell carcinoma;		
KW	Wilm's tumour; BIR 3 domain.		
OS			
XX	Unidentified.		
XX			
PN	WO2003040172-A2.		
XX			
PD	15-MAY-2003.		
PF	12-NOV-2002; 2002WO-CA001738.		
XX			
XX	09-NOV-2001; 2001US-0332300P.		
PR	08-APR-2002; 2002US-0370934P.		
PA	(AEGE-) AEGERA THERAPEUTICS INC.		
PI	Boudresault A, Korneluk RG, La Casse E, Liston P;		
XX			
DR	WPI; 2003-513532/48.		
PT	polypeptide capable of forming a complex with a polypeptide comprising a		
PT	baculovirus inhibitor of apoptosis repeat domain useful for treating		
PT	cancer and other neoplasms.		
PS			
XX	Disclosure; Fig 1B; 53pp; English.		
XX			
CC	This invention relates to a substantially pure polypeptide having a		
CC	length of less than 100 amino acids and capable of forming a complex with		
CC	a polypeptide that includes a baculovirus inhibitor of apoptosis repeat		
CC	(BIR) domain. The apoptosis pathway is known to play a critical role in		
CC	embryonic development, viral pathogenesis, cancer, autoimmune disorders		
CC	and neurodegenerative diseases. The failure of the apoptotic response has		
CC	been implicated in the development of cancer, autoimmune disorders (for		
CC	example systemic lupus erythematosus and multiple sclerosis) and viral		
CC	infections (including herpes virus, poxvirus and adenovirus. The		
CC	inhibitors of apoptosis (IAPs) are a family of proteins possessing one or		
CC	more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1		
CC	(CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy		
CC	terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and		
CC	-9 which are proteases involved in the initiation of apoptosis. Compounds		
CC	which inhibit the activity of IAPs may therefore have cytosstatic activity		
CC	through the enhancement of apoptosis. The polypeptide of the invention		
CC	are candidate peptide ligands for binding to the BIR domain of IAPs. They		
CC	may be useful for the treatment of cancer and other neoplasms, such as		
CC	leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular		
CC	cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma		
CC	and Wilm's tumour, and for enhancing apoptosis. The present sequence is		
CC	that of an unidentified inhibitor of apoptosis (IAP) protein IAP BIR3		
CC	domain which was used to demonstrate homology to human IAP protein BIR		
CC	domains to which the peptides of the invention are targeted to bind.		
XX			
XX			
SQ	Sequence 57 AA;		
Query Match	82.8%; Score 322; DB 7; Length 57;		
Best Local Similarity	94.6%; Pred. No. 2,1e-31;		
Matches	53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
QY	11 WIVSVNKKQLARAGFYALGSDQKXKCTHCGGGGLTDWKPSPDPWECHAKWYRGCKTL 66		
DB	2 WIVSVNKKQLARAGFYALGSDQKXKCTHCGGGGLTDWKPSPDPWECHAKWYRGCKTL 57		

RESULT 33
AD139821
ID AD139821 standard; protein; 53 AA.
AC AD139821;
XX 15-APR-2004 (first entry)
DT 15-APR-2004 (first entry)
DE Human NAIp BIRa region #1.
XX Inhibitor of apoptosis-like protein; iap; i1p; apoptosis; therapy;
XX cancer; cell immortalisation; cysteine protease; viral infection;
XX cytoskeletal; virucide; baculovirus iap-like repeat; BIR; human;
XX neural apoptosis inhibitory protein; NAIp.
XX Homo sapiens.
OS US6511828-B1.
PN 28-JAN-2003.
PD 31-MAY-1996; 96US-00657759.
PF 31-MAY-1996; 96US-00657759.
XX 31-MAY-1996; 96US-00657759.
PR 31-MAY-1996; 96US-00657759.
XX (ARCH-) ARCH DEV CORP.
PA Thompson CB, Duckett CS;
PI WPI; 2003-391256/37.
XX New inhibitor of apoptosis-like protein (i1p) and polynucleotide encoding
PT i1p, useful for inhibiting or stimulating apoptosis in target cells,
PT treating certain cancers, or sustaining host cell survival following
PT viral infection.
XX Example 2; SEQ ID NO 19; 42pp; English.
XX The present invention relates to inhibitor of apoptosis (iap)-like
XX proteins (i1p) and polynucleotides encoding such proteins. Sequences of
XX the invention are useful for inhibiting or stimulating apoptosis in
XX target cells or for treating certain cancers. They are also useful in the
XX immortalisation of cells for culture, for inhibiting the activation of
XX cysteine proteases and to sustain host cell survival following viral
XX infection. The i1p may also be used as a marker in gel separation
XX procedures or as a standard in protein concentration determinations. The
XX present sequence is human neural apoptosis inhibitory protein (NAIP)
XX baculovirus iap-like repeat (BIR) region.
SQ Sequence 53 AA;
Query Match 75.8%; Score 295; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EQIARAGFYALGSDGVKVCFCGGLTDMKPSDPMEOHAKWPGCKYL 66
Db 1 EQIARAGFYALGSDGVKVCFCGGLTDMKPSDPMEOHAKWPGCKYL 49
RESULT 34
ADB61829
ID ADB61829 standard; protein; 66 AA.
AC ADB61829;
XX 04-DEC-2003 (first entry)
DT 04-DEC-2003 (first entry)
DE Chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX baculovirus inhibitor of apoptosis repeat domain; BIR domain;
XX apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KM

KM autoimmune disorder; neurodegenerative disease; apoptotic response;
KM systemic lupus erythematosus; multiple sclerosis; viral infection;
KM herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KM HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KM caspase-9; cytoskeletal; neoplasm; leukemia; colon carcinoma;
KM cervical cancer; uterine cancer; testicular cancer;
KM small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KM Wilms tumour; BIR 3 domain; chicken.
XX Gallus gallus.
OS W02003040172-A2.
PN 15-MAY-2003.
PD 12-NOV-2002; 2002WO-CA001738.
PF 09-NOV-2001; 2001US-0332300P.
XX 08-APR-2002; 2002US-0370934P.
PR (AEGE-) AEGERA THERAPEUTICS INC.
XX Boudreaux A, Korneluk RG, La Casse E, Liston P;
XX WPI; 2003-513532/48.
XX Polypeptide capable of forming a complex with a polypeptide comprising a
XX baculovirus inhibitor of apoptosis repeat domain useful for treating a
XX cancer and other neoplasms.
XX Disclosure; Fig 1B; 53pp; English.
XX This invention relates to a substantially pure polypeptide having a
XX length of less than 100 amino acids and capable of forming a complex with
XX a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
XX (BIR) domain. The apoptosis pathway is known to play a critical role in
XX embryonic development, viral pathogenesis, cancer, autoimmune disorders
XX and neurodegenerative diseases. The failure of the apoptotic response has
XX been implicated in the development of cancer, autoimmune disorders (for
XX example systemic lupus erythematosus and multiple sclerosis) and viral
XX infections (including herpes virus, poxvirus and adenovirus. The
XX inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
XX more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
XX (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
XX terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
XX -9 which are proteases involved in the initiation of apoptosis. Compounds
XX which inhibit the activity of IAPs may therefore have cytostatic activity
XX through the enhancement of apoptosis. The polypeptides of the invention
XX are candidate peptide ligands for binding to the BIR domain of IAPs. They
XX may be useful for the treatment of cancer and other neoplasms, such as
XX leukemias, colon carcinoma, cervical cancer, uterine cancer, testicular
XX cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
XX and Wilms tumour, and for enhancing apoptosis. The present sequence is
XX that of the chicken inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
XX which was used to demonstrate homology to human IAP protein BIR domains
XX to which the peptides of the invention are targeted to bind.
SQ Sequence 66 AA;
Query Match 73.8%; Score 287; DB 7; Length 66;
Best Local Similarity 71.2%; Pred. No. 4.5e-27;
Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
QY 1 YEARIPTFGTWIYSVKNQOLARAGFYALGSDGVKVCFCGGLTDMKPSDPMEOHAKWY 60
Db 1 YERRIOTPLAWIYVKNKEHLARAGFYALGSDGVKVCFCGGLTDMKPSDPMEOHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKFL 66
RESULT 35

[illegible][illegible]

CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HAPI
 CC (CIAP2) and HAPI2 (CIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilms' tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein HAPI BIR3 domain
 CC against which the peptides of the invention are targeted to bind.

SO Sequence 68 AA;

Query Match 54.2%; Score 211; DB 7; Length 68;
 Best Local Similarity 57.4%; Pred. No. 8.2e-18;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTWIVS--VNKEQLARAGFYALGSDGVKVCFHGGGLTDMKPSDDPWEQHA 58
 DB 1 HAARFKTFPMWPSVLVNPEQLASAGFYVGNSDVVCFCDDGGLRCWESGDDPWVQHA 60
 QY 59 WYPCCKYL 66
 DB 61 WFPRCXYL 68

RESULT 39

ADO26592 ID ADO26592 standard; protein; 442 AA.

AC ADO26592;

DT 01-JUL-2004 (first entry)

XX Human APl2.

XX Chromosome translocation; malignancy;
 KM mucosa-associated lymphoid tissue-lymphoma associated translocation;
 KM MALT; MALT; primary cell transformation; apoptosis inhibitor 2; APl2;
 KM tumour; cytostatic; human.

OS Homo sapiens.

XX US6689875-B1.

PN 10-FEB-2004.

PD 26-MAY-2000; 2000US-00579692.

PF 09-JUN-1999; 99US-0138834P.

PR 09-JUN-1999; 99US-0138834P.

PS (VLA-A-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Dierlamm J, Baens M, Martijnen P;

XX WPI; 2004-141430/14.

DR N-PSDB; ADO26591.

XX New mucosa-associated lymphoid tissue-lymphoma associated translocation

PT protein, useful in diagnosing and treating tumors.

XX Disclosure; SEQ ID NO 58; 88pp; English.

CC The present invention relates to a method for characterisation of
 CC chromosome translocation T (11;18) (q21;q21) and its association with
 CC malignancies such as mucosa-associated lymphoid tissue (MALT)-lymphoma.
 CC Also disclosed are: the polynucleotide and polypeptide sequences for
 CC human mucosa-associated lymphoid tissue (MALT)-lymphoma associated
 CC translocation (MALT), and a novel mechanism of primary cell transformation

CC by expression of a fusion protein comprising at least apoptosis inhibitor
 CC 2 (APl2) fused to another protein such as MALT. The MALT polynucleotide and
 CC polypeptide sequences, and the method of the invention are useful in
 CC diagnosing and treating tumours. The present sequence represents human
 CC APl2.

XX Sequence 442 AA;

SO Query Match 54.2%; Score 211; DB 8; Length 442;
 Best Local Similarity 57.4%; Pred. No. 7e-17;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTWIVS--VNKEQLARAGFYALGSDGVKVCFHGGGLTDMKPSDDPWEQHA 58
 DB 255 HAARFKTFPMWPSVLVNPEQLASAGFYVGNSDVVCFCDDGGLRCWESGDDPWVQHA 314
 QY 59 WYPCCKYL 66
 DB 315 WFPRCXYL 322

RESULT 40

ABP72159 ID ABP72159 standard; protein; 557 AA.

AC ABP72159;

DT 22-APR-2003 (first entry)

XX Inhibitor of apoptosis protein CIAP2.

XX Inhibitor of apoptosis; CIAP2; apoptosis; cancer; leukaemia; lymphoma;
 KM neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX Unidentified.

OS WO200304606-A2.

PN 16-JAN-2003.

PD 03-JUL-2002; 2002WO-US021002.

PF 03-JUL-2001; 2001US-00898158.

PR (UYCO) UNIV COLUMBIA NEW YORK.

PS Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

DR N-PSDB; AB258104.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

PT treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 17A; 124pp; English.

CC The present sequence is the protein sequence of inhibitor of apoptosis
 CC protein CIAP2. The invention provides a nucleic acid, such as an
 CC antisense oligonucleotide, which specifically hybridises to a nucleic
 CC acid encoding an inhibitor of apoptosis protein, especially MIAPI, MIAPI2,
 CC MIAPI3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
 CC death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell, especially the
 CC use of a vector, liposome, or a mechanical or electrical means. The
 CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
 CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
 CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
 CC cell carcinoma and squamous cell carcinoma (all claimed)

XX Sequence 557 AA;

Query Match 54.2%; Score 211; DB 6; Length 557;
 Best Local Similarity 57.4%; Pred. No. 9.2e-17;

	Matches	39;	Conservative	6;	Mismatches	21;	Indels	2;	Gaps	1;
Qy	1	YEARI	FTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQYAK	58						
Db	255	HARFKTFEPMWSSVTLVNPBQLASAGFYVGNNSDDVKCFCCDGGILRCWESGDDPMVQYAK	314							
Qy	59	WYRGCKYL	66							
Db	315	WPRCEYL	322							

Search completed: June 15, 2005, 17:35:45
Job time : 116 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 17:32:02 ; Search time 31 Seconds
(without alignments)
158,930 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389

Sequence: 1 YEAR1PTFGTWIYSVNKEOL.....KPSHPDWEHAKWPGCKYL 66

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

- 1: Issued Patents AA:*
- 2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/BACKFILE1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	66	2	US-08-511-485-25
2	389	100.0	66	4	US-09-201-936-25
3	389	100.0	66	4	US-09-011-356-25
4	389	100.0	66	4	US-09-201-932-25
5	389	100.0	236	3	US-09-239-867-4
6	389	100.0	236	4	US-10-024-433-4
7	389	100.0	497	2	US-08-511-485-4
8	389	100.0	497	3	US-09-212-971-4
9	389	100.0	497	3	US-08-800-929A-4
10	389	100.0	497	3	US-09-617-053A-4
11	389	100.0	497	4	US-08-657-759-2
12	389	100.0	497	4	US-09-201-936-4
13	389	100.0	497	4	US-09-011-356-4
14	389	100.0	497	4	US-09-672-717-219
15	389	100.0	497	4	US-09-201-932-4
16	389	100.0	497	4	US-09-949-016-6032
17	366	94.1	66	2	US-08-511-485-24
18	366	94.1	66	4	US-09-201-936-24
19	366	94.1	66	4	US-09-011-356-24
20	366	94.1	66	4	US-09-201-932-24
21	366	94.1	496	2	US-08-511-485-10
22	366	94.1	496	3	US-09-212-971-10
23	366	94.1	496	3	US-08-800-929A-10
24	366	94.1	496	3	US-09-617-053A-10
25	366	94.1	496	4	US-09-201-936-10
26	366	94.1	496	4	US-09-011-356-10
27	366	94.1	496	4	US-09-672-717-225

28	366	94.1	496	4	US-09-201-932-10	Sequence 10, Appl
29	347	89.2	236	3	US-09-121-979-4	Sequence 4, Appl
30	347	89.2	236	3	US-09-332-319-4	Sequence 4, Appl
31	347	89.2	236	3	US-09-239-867-2	Sequence 2, Appl
32	347	89.2	236	4	US-10-024-433-2	Sequence 2, Appl
33	295	75.8	53	4	US-08-657-759-19	Sequence 19, Appl
34	249	64.0	50	3	US-08-975-080-28	Sequence 29, Appl
35	249	64.0	50	3	US-08-975-080-32	Sequence 29, Appl
36	249	64.0	50	3	US-08-975-080-32	Sequence 29, Appl
37	249	64.0	50	4	US-10-138-618-28	Sequence 28, Appl
38	249	64.0	50	4	US-10-138-618-32	Sequence 29, Appl
39	249	64.0	50	4	US-10-138-618-32	Sequence 29, Appl
40	211	54.2	68	2	US-08-511-485-26	Sequence 26, Appl
41	211	54.2	68	4	US-09-201-936-26	Sequence 26, Appl
42	211	54.2	68	4	US-09-011-356-26	Sequence 26, Appl
43	211	54.2	68	4	US-09-201-932-26	Sequence 26, Appl
44	211	54.2	442	4	US-09-579-692B-58	Sequence 58, Appl
45	211	54.2	604	2	US-08-511-485-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-25
Sequence 25, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-25
Query Match 100.0%; Score 389; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YEAR1PTFGTWIYSVNKEOLARAGFYALGEGDYKCFHCGGLTDWKPSSDPWEHAKWY 60
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Db 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
Db 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
Db 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4
US-09-201-932-25
; Sequence 25, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2,4e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
Db 1 YEARIFFTGWTWISVKNKQLARAGFYALGEGDVKYKCFHCGGGLTDMKPSDPMEOHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 5
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
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; PRIOR FILING DATE: 1998-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-239-867-4

Query Match 100.0%; Score 389; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.1e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 60
 Db 4 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 63

Qy 61 PGCKYL 66
 Db 64 PGCKYL 69

RESULT 6
 US-10-024-433-4
 ; Sequence 4, Application US/10024433
 ; Patent No. 6797473
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Korneluk et al.
 ; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
 ; FILE REFERENCE: 07891/018002
 ; CURRENT APPLICATION NUMBER: US/10/024,433
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/239,867
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-433-4

Query Match 100.0%; Score 389; DB 4; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.1e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 60
 Db 4 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 63

Qy 61 PGCKYL 66
 Db 64 PGCKYL 69

RESULT 7
 US-08-511-485-4
 ; Sequence 4, Application US/08511485
 ; Patent No. 5919912
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Baird, Stephen
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA

; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/511,485
 ; FILING DATE: 04-AUG-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 07540/002001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 497 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: both
 ; MOLECULE TYPE: protein
 US-08-511-485-4

Query Match 100.0%; Score 389; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 60
 Db 265 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKVCFHCGGGLTDMKPSBDPMEQHAAMY 324

Qy 61 PGCKYL 66
 Db 325 PGCKYL 330

RESULT 8
 US-09-212-971-4
 ; Sequence 4, Application US/09212971B
 ; Patent No. 6107041
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Mackenzie, Alexander E.
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K.
 ; APPLICANT: Pratt, Christine
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009002
 ; CURRENT APPLICATION NUMBER: US/09/212,971B
 ; CURRENT FILING DATE: 1998-12-16
 ; EARLIER APPLICATION NUMBER: 60/017,354
 ; EARLIER FILING DATE: 1996-04-26
 ; EARLIER APPLICATION NUMBER: 60/030,590
 ; EARLIER FILING DATE: 1996-11-14
 ; EARLIER APPLICATION NUMBER: 08/800,929
 ; EARLIER FILING DATE: 1997-02-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-212-971-4

Query Match 100.0%; Score 389; DB 3; Length 497;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;

REFERENCE/DOCKET NUMBER: ARCD:220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-2

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2,8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 60
DB 265 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 12
US-09-201-936-4
Sequence 4, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2,8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 60
DB 265 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 13
US-09-011-356-4
Sequence 4, Application US/09011356A
Patent No. 6556704
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
EARLIER FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-011-356-4

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2,8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 60
DB 265 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 14
US-09-672-717-219
Sequence 219, Application US/09672717
Patent No. 6673917
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Lacasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Theret
FILE REFERENCE: 07891/025001
CURRENT APPLICATION NUMBER: US/09/672,717
EARLIER FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 219
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-672-717-219

Query Match 100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2,8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 60
DB 265 YEARIFFGTWIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSDDPMEQHAKWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 15

```
US-09-201-932-4
; Sequence 4, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Lister, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-932-4

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 16
US-09-949-016-6032
; Sequence 6032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6032
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6032

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330
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Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 17
US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/08/511,485
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-511-485-24

Query Match      94.1%; Score 366; DB 2; Length 66;
Best Local Similarity 95.5%; Pred. No. 2.7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 60
Db      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 60
Qy      61 PGCKYL 66
Db      61 PGCKYL 66

RESULT 18
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Lister, Peter
US-09-201-936-24

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 60
Db      265 YEARIFFTGWTIVSVNKEQLARAGFYALGSDGDKVCFHCGGGLTDMKPSBDPWEQHAQKY 324
Qy      61 PGCKYL 66
Db      325 PGCKYL 330
```

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 66
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-24

Query Match 94.1%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 2,7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60
Db 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60

Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 19

US-09-011-356-24
Sequence 24, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 66
TYPE: PRT
ORGANISM: Mus musculus
US-09-011-356-24

Query Match 94.1%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 2,7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60
Db 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60

Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 20

US-09-201-932-24
Sequence 24, Application US/09201932A
Patent No. 6689562
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003004
CURRENT APPLICATION NUMBER: US/09/201,932A
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 66
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-932-24

Query Match 94.1%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 2,7e-41;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60
Db 1 YEARIFTGWTWISVKNQOLARAGFYALGEGDKVCFHCGGGLTDMKPSDDPWEOHAKMY 60

Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 21

US-08-511-485-10
Sequence 10, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617, 053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMEOHAKMY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 25
US-09-201-936-10
Sequence 10, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMEOHAKMY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKY 323
QY 61 PGCKYL 66

DB 324 PGCKYL 329

RESULT 26
US-09-011-356-10
Sequence 10, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-011-356-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMEOHAKMY 60
DB 264 YEARIVFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMDOHAKY 323

QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 27
US-09-672-717-225
Sequence 225, Application US/09672717
Patent No. 6673917
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Therapeutic
FILE REFERENCE: 07891/025001
CURRENT APPLICATION NUMBER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 225
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-672-717-225

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVYKCFHCGGGLTDMKPSDPMEOHAKMY 60

Db 264 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 323
QY 61 PGCKYTL 66
|||
Db 324 PGCKYTL 329

RESULT 28
US-09-201-932-10
; Sequence 10, Application US/09201932A
; Patent No. 6689562
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baild, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932A
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-932-10

Query Match 94.1%; Score 366; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 3.3e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 60
|||
Db 264 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 323

QY 61 PGCKYTL 66
|||
Db 324 PGCKYTL 329

RESULT 29
US-09-121-979-4
; Sequence 4, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-979-4

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 60
|||
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLANWKPEDPMEOHAKKY 63
QY 61 PGCKYTL 66
|||
Db 64 PGCKYTL 69

RESULT 30
US-09-332-319-4
; Sequence 4, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-332-319-4

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 60
|||
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLANWKPEDPMEOHAKKY 63
QY 61 PGCKYTL 66
|||
Db 64 PGCKYTL 69

RESULT 31
US-09-239-867-2
; Sequence 2, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-2

Query Match 89.2%; Score 347; DB 3; Length 236;
Best Local Similarity 84.8%; Pred. No. 4.4e-38;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMEOHAKKY 60
|||
Db 4 YEARITFTGWTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLANWKPEDPMEOHAKKY 63

QY 61 PGCKYL 66
 DB 64 PGCKYL 69

RESULT 32
 US-10-024-433-2
 ; Sequence 2, Application US/10024433
 ; Patent No. 6797473
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Korneluk et al.
 ; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
 ; FILE REFERENCE: 07891/018002
 ; CURRENT APPLICATION NUMBER: US/10/024,433
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 09/239,867
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-433-2

Query Match 89.2%; Score 347; DB 4; Length 236;
 Best Local Similarity 84.8%; Pred. No. 4,4e-38;
 Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIPTGWTIVSYNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAQKY 60
 DB 4 YEARIPTGWTIVSYNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAQKY 63
 QY 61 PGCKYL 66
 DB 64 PGCKYL 69

RESULT 33
 US-08-657-759-19
 ; Sequence 19, Application US/08657759
 ; Patent No. 6511828
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Craig B.
 ; APPLICANT: Duckett, Colin S.
 ; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
 ; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/657,759
 ; FILING DATE: 31-MAY-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: ARCD:220
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 53 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-657-759-19

Query Match 75.8%; Score 295; DB 4; Length 53;
 Best Local Similarity 100.0%; Pred. No. 5.9e-32;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EQARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAQKYPGCKYL 66
 DB 1 EQARAGFYALGEGDKVCFHCGGLTDMKPSDPEQHAQKYPGCKYL 49

RESULT 34
 US-08-975-080-28
 ; Sequence 28, Application US/08975080
 ; Patent No. 6245523
 ; GENERAL INFORMATION:
 ; APPLICANT: Altieri, Dario C.
 ; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 ; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 ; STREET: 1800 M Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036-5869
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,080
 ; FILING DATE: 20-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/031,435
 ; FILING DATE: 20-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adler, Reid G.
 ; REGISTRATION NUMBER: 30,988
 ; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-467-7000
 ; TELEFAX: 202-467-7176
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 50 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-975-080-28

Query Match 64.0%; Score 249; DB 3; Length 50;
 Best Local Similarity 100.0%; Pred. No. 7.2e-26;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCFHCGGLTDMKPSDPEQHAQKYPGCKYL 66
 DB 1 ALGEGDKVCFHCGGLTDMKPSDPEQHAQKYPGCKYL 40

RESULT 35
 US-08-975-080-29
 ; Sequence 29, Application US/08975080
 ; Patent No. 6245523

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-29

Query Match 64.0%; Score 249; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7,2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVRCFHGGGLTDWKPSDDPWEQHAKYPGCKYL 66
Db 1 ALGEGDKVRCFHGGGLTDWKPSDDPWEQHAKYPGCKYL 40

RESULT 36
US-08-975-080-32
Sequence 32, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-32

Query Match 64.0%; Score 249; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7,2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVRCFHGGGLTDWKPSDDPWEQHAKYPGCKYL 66
Db 1 ALGEGDKVRCFHGGGLTDWKPSDDPWEQHAKYPGCKYL 40

RESULT 37
US-10-138-618-28
Sequence 28, Application US/10138618
Patent No. 6800737
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 40

RESULT 38
US-10-138-618-29
Sequence 29, Application US/10138618
Patent No. 6800737

GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.

TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 40

RESULT 39
US-10-138-618-32
Sequence 32, Application US/10138618
Patent No. 6800737

GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.

TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 40

RESULT 39
US-10-138-618-32
Sequence 32, Application US/10138618
Patent No. 6800737

GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.

TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match 64.0%; Score 249; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 66
DB 1 ALGEGDKVCKFCGCGGLTDWKPSEDPWEQHAQKYPGCKYL 40

RESULT 40
US-08-511-485-26
Sequence 26, Application US/08511485
Patent No. 5919912

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
AND DETECTION METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-26

Query Match 54.2%; Score 211; DB 2; Length 68;
 Best Local Similarity 57.4%; Pred. No. 1.2e-20;
 Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YBARIFTFGTWYS--VNKEQLARAGFYALGEGDKVKCFHGGGLTDMKPSDEDFWEQAK 58
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 HAARFKTFEWMPSVVLNPEQLASAGFYVGNSDVXCFCCDGLRCMESGDDPMVQAK 60
 QY 59 WYPCCKYL 66
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 WFPRCXYL 68

Search completed: June 15, 2005, 17:53:09
 Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: June 15, 2005, 17:27:02 / Search time 23.5 Seconds
(without alignments)
270.226 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIPTFGTWIYSVNKEQL.....KPSEDPWEQHAQWPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	497	2	S69544 apoptotic inhibitor
2	211	54.2	604	2	S68449 apoptotic inhibitor
3	209	53.7	358	2	UC5964 apoptotic inhibitor
4	205	52.7	268	2	T10304 inhibitor of apopt
5	205	52.7	268	2	A53989 apoptotic-inhibiti
6	198	50.9	618	2	S68450 apoptotic inhibitor
7	190	48.8	275	2	A45679 inhibitor-of-apopt
8	188	45.3	298	2	JC7568 kidney inhibitor o
9	177.5	45.6	1232	2	A55478 neuronal apoptosis
10	174.5	44.9	1447	2	T42628 apoptotic inhibitor
11	162	41.6	496	2	S68452 apoptotic inhibitor
12	162	41.6	497	2	S69545 apoptotic inhibitor
13	144	37.0	208	2	T03183 probable apoptosis
14	139	35.7	150	2	T28409 ORF MSV248 probabl
15	125	32.1	275	2	T10310 apoptotic-inhibiti
16	115.5	29.7	4845	2	T31067 BIR repeat contain
17	111	28.5	286	2	D36828 orf13 protein - Au
18	109	28.0	292	2	T41772 IAP1 orf27 - Bomby
19	101	26.0	155	2	T30489 apoptotic inhibitor
20	100	25.7	155	2	T37471 apoptotic inhibitor
21	97	24.9	308	2	T37474 ORF MSV242 probabl
22	87.5	22.5	329	2	T28403 ORF MSV242 probabl
23	87.5	22.5	997	2	T43523 A55R protein - fl
24	79.5	20.4	564	2	C42523 A55R protein - vac
25	79.5	20.4	564	2	J01792 Salp17R protein -
26	66	17.0	576	1	ACPPA2 nicotinic acetylch
27	65	16.7	249	2	H72858 apoptotic inhibitor
28	65	16.7	444	2	T15907 hypothetical prote
29	65	16.7	1808	2	T15099 hypothetical prote

30	64.5	16.6	557	2	S12359 nicotinic acetylch
31	64.5	16.6	737	2	PQ0219 RNA-2 polypeptide
32	63.5	16.3	506	2	S13720 coat protein - ara
33	63.5	16.3	607	2	T39823 hypothetical prote
34	63	16.2	234	2	T30427 probable apoptosis
35	62.5	16.1	324	2	S39502 vegetative storage
36	62.5	16.1	532	2	A32751 speract receptor p
37	62	15.9	249	2	T41814 IAP2 orf71 - Bomby
38	62	15.9	474	2	S28419 lamin B-3 - mouse
39	62	15.9	592	2	B48315 nicotinic acetylch
40	61	15.7	511	2	T43634 hypothetical prote
41	61	15.7	534	2	T25720 hyaluronate lyase
42	61	15.7	776	2	T29064 probable dna-3-met
43	60	15.4	204	2	H70609 MHC class II histo
44	60	15.4	246	2	T50127 MHC class II histo
45	60	15.4	252	2	I50126 MHC class II histo

ALIGNMENTS

```
RESULT 1
S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69544; S68451
R:Duckett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-References: UNIPROT:P98170; EMBL:U32974; NID:G1016687; PID:AC50518.1; PID:G1016687
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:Cross-References: EMBL:U45880; NID:G1184319; PID:AA50373.1; PID:G1184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWIYSVNKEQLRAGFYALGSGDKVCFHCGGGLTDMKPSEDPWEQHAQWY 60
DB 265 YEARIPTFGTWIYSVNKEQLRAGFYALGSGDKVCFHCGGGLTDMKPSEDPWEQHAQWY 324

QY 61 PGCKYL 66
DB 325 PGCKYL 330

RESULT 2
S68449
apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
```

Nature 379, 343-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by Nalp and a related family of IAPs
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:PAC50371.1; PID:g118185
A:Function:
A:Description: apoptotic suppressor
A:Keywords: apoptosis; zinc finger
A:553-597/Domain: RING finger homology <RNG>

Query Match	54.2%	Score 211;	DB 2;	Length 604;
Best Local Similarity	57.4%	Pred. No. 2.9e-16;		
Matches 39;	Conservative 6;	Mismatches 21;	Indels 2;	Gaps 1;

Query Match	54.2%	Score 211;	DB 2;	Length 604;
Best Local Similarity	57.4%	Pred No. 2.9e-16;		
Matches	39;	Conservative	6;	Mismatches 21; Indels 2; Gaps 1.

QY	1	Y	E	A	R	T	G	T	W	I	Y	--	V	N	K	E	Q	L	A	R	G	F	A	L	E	G	D	R	Y	K	C	F	H	G	G	G	I	T	M	K	S	E	D	P	W	E	O	H	A	K	58		
Db	255	H	A	A	R	K	T	E	F	N	N	S	S	V	L	N	P	E	O	L	A	S	G	F	Y	V	G	N	S	D	V	K	C	F	C	D	D	G	R	C	W	E	S	G	D	D	P	W	O	H	A	K	314
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			

QY	59	W	P	G	C	K	Y	L	66	
Db	315	W	P	P	R	C	E	Y	L	322
		:	:	:	:	:	:	:	:	

RESULT 3
JC5964

apoptosis inhibitor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C/Accession: J05964
R/Steinhilb, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A./Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap) fam
A./Reference number: J05964; PMID:98162622; PMID:9501011
A./Accession: J05964
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-358 <STE>
A./Cross-references: UNIPROT:O62640; GB:U79142; NID:G2957174; PIDN:AAC39177.1; PID:G2957174
A./307-351/Domain: RING finger homology <RNR>

Query Match	53.7%	Score 209;	DB 2;	Length 358;
Best Local Similarity	55.9%;	Pred. No. 2.9e-16;		
Matches 38;	Conservative 7;	Mismatches 21;	Indels 2;	Gaps 1;

QY 1 YEAIIPFEGTIIYS--VNKEQLARAGFYALGEGSKVCFHCGGGLITMKPSBEDMECHAK 58
Db 90 YAAAFKTFPCNPPSIPVHPBOLASNGFYTMGSHSDVKCFCCDGGILRCWESGDPEVHAHAK 149
QY 59 WYPGCKYL 66
Db 150 WFPRCGYL 157

RESULT 4
T10304

RESULT 4
 T10304
 Inhibitor of apoptosis protein 3 - *Oryzia pseudotubugata* nuclear polyhedrosis virus
 C/Species: *Oryzia pseudotubugata* nuclear polyhedrosis virus, OPMFV
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
 C/Accession: T10304
 R:/Authors, C.A.; Russell, R.R.; Funk, C.U.; Evans, J.; Harwood, S.; Rohmann, G.F.
 Virology 229, 381-399, 1997
 A/Title: The sequence of the *Oryzia pseudotubugata* multinucleocapsid nuclear polyhedrosis
 A/Reference number: Z17011; MUID:91271300; PMID:9156251

A:Accession: J10304
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-References: EMBL:U075930; NID:G2934903; PIDD:AA059034.1; PIDD:91911281
C:Superfamily: vital apoptosis inhibitor IAP; RING finger homology
C:217-261/domain: RING finger homology <REN>

Query Match	52.7%;	Score 205;	DB 2;	Length 268;
Best Local Similarity	50.0%;	Pred. No. 6.3e-16;		
Matches 33; Conservative	13;	Mismatches 18;	Indels 2;	Gaps 1

3 ARIPTFGTWIYSVNK--EQLRAGFYALGEGDKVKCFHCGGGITDWMKSESDPMEQIAKNY 60
||:|||:::|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
113 ARLRFAEMWRGLKORPEELAEAGFYYTGQDKTRCCCDGIGAKMDEPDAPMOOHARMY 172

QY 61 PGCKYL 66
|:|:
173 DRCEYV 178

RESULT 5
A53989

RESULT 5
 A53989
 Apoptosis-inhibiting protein - *Orygia pseudosynagata* multicapsid nuclear polyhedrosis virus
 C:Species: *Orygia pseudosynagata* multicapsid nuclear polyhedrosis virus, OpMNPV
 C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C:Accession: A53989
 J:Virion: 60, 2521-2528, 1994
 A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide
 A:Reference number: A53989; MUID:94187094; PMID:8139034
 A:Accession: A53989

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BIR>
A:Cross-references: UNIPROT:P41437, GB:L22564, NID:g45611, PID:g456114
A:Note: authors translated the codon TGG for residue 28 as Ty, GAC for residue 50 as Asp
C:Superfamily: viral apoptosis inhibitor IAP, RING finger homology
F:217-261/Domains: RING finger homology <RRN>
F:217-261/Domains: RING finger homology

Query Match 52.7%; Score 205; DB 2; Length 268;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

3 ARIFFTGWTIYSVKK--EQIARAGFYALGEGDKVKCFHCGGLTDWKPSEDPMQOHAKRY 60
||:|||:::|||||:|||||:|||||:|||||:
113 ARLTFAMPRGLKORPEELIENAGFFYTGODKTCTCCDGGIKDWEDDAPAOOHARY 172

2Y 61 PGCKYL 66
|::|:
2b 173 DRCEYV 178

RESULT 6
S688450
Species: Homo sapiens (man)
Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
Accession: S688450

1:Rilston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
 2:Suppression of apoptosis in mammalian cells by NAIp and a related family of IAP
 3:Structure 379, 349-353, 1996
 4:Title: Suppression of apoptosis in mammalian cells by NAIp and a related family of IAP
 5:Reference number: A58182; MUID:96149249; PMID:8552191
 6:Accession: S68450
 7:Status: nucleic acid sequence not shown

```

>Molecule type: mRNA
>Residues: 1-618 <LIS>
>Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:g1164317; PIDD:AA050372.1; PIDD:g1164318
>Function:
>Description: apoptotic suppressor
>Keywords: apoptosis; zinc finger
>2567-611/Domain: RING finger homology <RNG>
>2567-611/Domain: RING finger homology <RNG>

```

Query Match	50.9%;	Score 198;	DB 2;	Length 618;
Best Local Similarity	52.9%;	Pred. No. 9.2e-15;		
Matches	36;	Conservative	9;	Mismatches 21;
				Indels 2;
				Gaps 1;

1 YEARI FTG TWIS--VNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSEDPMWEQHA 58
 : :: : | | | | | | | | : | | | | | : : :: : |||
269 HAARMRTWMPSPVPVOEQLAAGFYVGRNDVKCFCGDGLGCMESGDPPWEVHA 38

Qy 59 WYPCCKYL 66
|:|:|:
Db 329 WPPKCEFL 336

RESULT 7

A45679

Inhibitor-of-apoptosis polypeptide (IAP) - *Cydia pomonella* granulosis virus CpGVC/Species: *Cydia pomonella* granulosis virus CpGV

C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: A45679

R/Crook, N.E.; Miller, L.K.

J. Virol. 67, 2168-2174, 1993

A/Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.

A/Residues: 1-275 <CRO>

A/Cross-references: UNIPROT:P41436; GB:L05494; NID:G289583; PIDN:AAA43835.1; PID:G289584

A/Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P:127015)

C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 48.8%; Score 190; DB 2; Length 275;

Best Local Similarity 47.0%; Pred. No. 3.4e-14;

Matches 31; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

Qy 3 ARIFFTGTV--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDEPWEQHAQW 60

Db 110 ARVASFNNPRCMKQREBQMDAGFYTYGYDNTKCFYCDGLXDMBEDVPEQHVHWF 169

Qy 61 PGCKYL 66

Db 170 DRCAIV 175

RESULT 8

JC7568

kidney inhibitor of apoptosis protein - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JC7568

R/Lin, J.H.; Deng, G.; Huang, Q.; Morse, J.

Biochem. Biophys. Res. Commun. 279, 820-831, 2000

A/Title: KIAA, a novel member of the inhibitor of apoptosis protein family.

A/Reference number: JC7568; MUID: 21092523; PMID:11162435

A/Contents: Fetal kidney

A/Accession: JC7568

A/Molecule type: mRNA

A/Residues: 1-298 <LIN>

A/Cross-references: UNIPROT:Q96CA5

C/Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays

C/Genetics:

A/Gene: klap

A/Map position: 20q13.3

C/Keywords: apoptosis

Query Match

Best Local Similarity 48.3%; Score 188; DB 2; Length 298;

Matches 33; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

Qy 2 EARIFFTGTV--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDEPWEQHAQW 59

Db 88 ELRLASFYDWPDLTAEPPELLAAAGFHTGHQDKVRCFCYGLQSWKRGDDPWTETAKW 147

Qy 60 YPGCKYL 66

Db 148 WPPKCEFL 154

RESULT 9

A55478
neutroal apoptosis inhibitory protein - human
N/Alternate names: NAIP
C/Species: Homo sapiens (man)
C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001

C/Accession: A55478

R/Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yaraghi, Z.; Farahani, R.; Baird, S

d, T.O.; de Jong, P.J.; Suth, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.

Cell 80, 167-178, 1995

A/Title: The gene for neutroal apoptosis inhibitory protein is partially deleted in indi

A/Reference number: A55478; MUID:5112344; PMID:781303

A/Accession: A55478

A/Molecule type: mRNA

A/Residues: 1-1232 <ROY>

A/Cross-references: GB:U19251

C/Genetics:

A/Gene: GDB:SMA@; SMA

A/Cross-references: GDB:120378; OMIM:600354; OMIM:253300

A/Map position: 5q12.2-5q13

C/Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote

F/94-110/Domain: transmembrane #status predicted <TM1>

F/470-477/Region: nucleotide-binding motif A (P-loop)

F/479-496/Domain: transmembrane #status predicted <TM2>

F/476/Binding site: ATP (Lys) #status predicted

F/618,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 45.6%; Score 177.5; DB 2; Length 1232;

Best Local Similarity 42.6%; Pred. No. 4e-12;

Matches 29; Conservative 16; Mismatches 20; Indels 3; Gaps 1;

Qy 2 EARIFFTGTV--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDEPWEQHAQW 58

Db 160 EARLASFRNPFYVGISPCVLSBAGFVFTGKQDVTQCFSCGGLGMBEGDDPWKEHAQW 219

Qy 59 WYPCCKYL 66

Db 220 WPPKCEFL 227

RESULT 10

T42628

neutroal apoptosis inhibitory protein 2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T42628

R/Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.

Mamm. Genome 10, 761-763, 1999

A/Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murin

A/Reference number: Z22179; MUID:9315342; PMID:10384056

A/Accession: T42628

A/Molecule type: mRNA

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-1447 <YAR>

A/Cross-references: UNIPROT:Q9QUK4; EMBL:AF102871; NID:G3860228; PID:G3860229; PIDN:AAC77

C/Genetics:

A/Gene: Naip2

Query Match 44.9%; Score 174.5; DB 2; Length 1447;

Best Local Similarity 42.6%; Pred. No. 1e-11;

Matches 29; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

Qy 2 EARIFFTGTV--IYSVNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSDEPWEQHAQW 58

Db 160 EARLESFEDMPFRAHGSFVLAAGFVFTGKQDVTQCFSCGGLGMBEGDDPWKEHAQW 219

Qy 59 WYPCCKYL 66

Db 220 WPPKCEFL 227

RESULT 11

S68452

apoptosis inhibitor diap - fruit fly (*Drosophila melanogaster*)

C/Species: Drosophila melanogaster
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: S68452; S78528
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A/Title: Suppression of apoptosis in mammalian cells by NMRP and a related family of IAP
A/Reference number: A58182; MUID:96142249; PMID:8552191
A/Accession: S68452
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-496 <LIS>
A/Cross-references: UNIPROT:Q24307; EMBL:U45881; NID:g1184313; P1DN:AA646988.1; P1D:g1184313; R/Baird, S.D.
Submitted to the EMBL Data Library, January 1996
A/Reference number: S78528
A/Accession: S78528
A/Molecule type: mRNA
A/Residues: 1-36; 'AT', '37', 'K', '39', 'L', '41-44', 'H', '46-58', 'Q', '60-412', 'A', '414-427', 'A', '429-496 <C/Genetics: 8
A/Cross-references: FlyBase:FBgn0015247
C/Function:
A/Description: apoptotic suppressor
C/Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C/Keywords: apoptosis; zinc finger
F/445-489/Domain: RING finger homology <RNG>

Query Match 41.6%; Score 162; DB 2; Length 496;
Best Local Similarity 43.3%; Pred. No. 9.6e-11;
Matches 29; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

Qy 2 EARIFFTGTVWS--VNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPWEQIAKV 59
Db 211 DARRTRTFDTPISNIQPASALAGLYYQKIGDQVRCFHCNIGLRWQKDEPFWEHAKV 270

Qy 60 YPGCKYL 66
Db 271 SPKQCFV 277

RESULT 12
S69545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S69545
R/Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C. EMBO J. 15, 2685-2694, 1996
A/Title: A conserved family of cellular genes related to the baculovirus iap gene and er
A/Reference number: S69544; MUID:96256286; PMID:8654366
A/Accession: S69545
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-497 <DUC>
A/Cross-references: UNIPROT:Q24307; EMBL:U32373; NID:g1019116; P1DN:AA647155.1; P1D:g1019116; C/Genetics: 9
A/Note: IAP
C/Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F/446-490/Domain: RING finger homology <RRN>

Query Match 41.6%; Score 162; DB 2; Length 497;
Best Local Similarity 43.3%; Pred. No. 9.6e-11;
Matches 29; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

Qy 2 EARIFFTGTVWS--VNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPWEQIAKV 59
Db 213 DARRTRTFDTPISNIQPASALAGLYYQKIGDQVRCFHCNIGLRWQKDEPFWEHAKV 272

Qy 60 YPGCKYL 66
Db 273 SPKQCFV 279

RESULT 13
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C/Species: Chilo iridescent virus
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 15-Mar-2004
C/Accession: T03183
R/Barr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A/Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A/Reference number: Z14834; MUID:98141693; PMID:9482589
A/Accession: T03183
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-208 <BAH>
A/Cross-references: EMBL:AF003534; NID:g2738385; P1DN:AA894481.1; P1D:g2738454
F/159-202/Domain: RING finger homology <RRN>

Query Match 37.0%; Score 144; DB 2; Length 208;
Best Local Similarity 45.0%; Pred. No. 4.6e-09;
Matches 27; Conservative 14; Mismatches 17; Indels 2; Gaps 1;

Qy 1 YEARIFFGTWISV--NKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPWEQIAKV 58
Db 37 YDERINSFQWMPQLRPSKQLSRAGTYINIGDQVCFYCDLKTAKMKRSDNPFEBHAK 96

RESULT 14
T28409
ORF MSY248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomop
C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T28409
R/Alonso, C.L.; Tulman, E.R.; Lu, Z.; Ona, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28409
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-150 <AFO>
A/Cross-references: UNIPROT:Q2YV04; EMBL:AF063866; NID:g4049647; P1DN:AA697724.1; P1D:g4049647; C/Genetics: 8
A/Note: MSY248

Query Match 35.7%; Score 139; DB 2; Length 150;
Best Local Similarity 34.8%; Pred. No. 1.2e-08;
Matches 24; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

Qy 2 EARIFFTGTV---IYSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPWEQIAKV 57
Db 17 QSRINSYENWPISLFFKINR--LCEAGFPYTNIGDITVCFCGLKITKMWLYNDPWIHES 74

Qy 58 KMYPGCKYL 66
Db 75 KMSPNCTNYI 83

RESULT 15
T10310
apoptosis-inhibiting protein 1 - Oryza pseudocausata nuclear polyhedrosis virus
C/Species: Oryza pseudocausata nuclear polyhedrosis virus, OpkmPV
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C/Accession: T10310
R/Alrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
A/Title: The sequence of the Oryza pseudocausata multinnucleocapsid nuclear polyhedrosis
A/Reference number: Z17011; MUID:97271300; PMID:9126251
A/Accession: T10310
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-275 <AHR>
A/Cross-references: EMBL:U75930; NID:g2934903; P1DN:AA639040.1; P1D:g1911287
C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F,223-268/Domain: RING finger homology <RRN>

Query Match 32.1%; Score 125; DB 2; Length 275;
Best Local Similarity 36.4%; Pred. No. 9e-07;
Matches 24; Conservative 11; Mismatches 29; Indels 2; Gaps 1;

QY 3 ARIFPTGWTIVSN--KEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWY 60
DB 128 ARARPTFHMPALNALTHDIAEAGMFTMLGDETFACFCDCRVRDMLPGDDPQWQHLALAN 187

QY 61 PGCKYL 66
DB 188 PGCFYFV 193

RESULT 16

BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31067

R/Hausser, H.P.; Bardroff, M.; Pyrowolskie, G.; Jentsch, S.

J. Cell Biol. 141, 1415-1422, 1998

A/Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.

A/Reference number: Z20963; MUID:98292517; PMID:9628897

A/Accession: T31067

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-4845 <HAU>

A/Cross-references: UNIPROT:O88738; EMBL:Y1267; NID:9331989; PIDN:CAA76720.1; PID:9331

A/Note: localized to the Golgi compartment and the vesicular system

C/Keywords: membrane-associated protein

Query Match 29.7%; Score 115.5; DB 2; Length 4845;
Best Local Similarity 31.3%; Pred. No. 0.00019;
Matches 21; Conservative 14; Mismatches 25; Indels 7; Gaps 2;

QY 7 TFGTIVTS---VNKEQLARAGFY---ALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWY 59
DB 267 TFGTIVTS---VNKEQLARAGFY---ALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWY 326

QY 60 YPGCKYL 66
DB 327 SPNCPFV 333

RESULT 17

orf13 protein - Autographa californica nuclear polyhedrosis virus

C/Species: Autographa californica nuclear polyhedrosis virus, AcNPV
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: D36828; C72853

R/Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.

Virology 191, 1003-1008, 1992

A/Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica VP8 of rofavivirus.

A/Reference number: A44221; MUID:93079853; PMID:1333113

A/Accession: D36828

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 <BRA>

A/Cross-references: UNIPROT:P41435; GB:S52569

R/Araya, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A/Reference number: A72850; MUID:94303173; PMID:8030224

A/Accession: C72853

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-199, 'L', 201-286 <AYR>

A/Cross-references: GB:L22858; NID:9510708; PIDN:AAA6657.1; PID:9559096

C/Genetics:

A/Gene: Ac-IAP1

C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 28.5%; Score 111; DB 2; Length 286;
Best Local Similarity 38.3%; Pred. No. 3.7e-05;
Matches 18; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 20 LABAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWYPCCKYL 66
DB 153 IAEAGLFYTGGRGDETVCFDCDCVRDWMHTEDTQGHAAENPQCFYFV 199

RESULT 18

IAP1 orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C/Species: Bombyx mori nuclear polyhedrosis virus, BmNPV
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41772

R/Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A/Reference number: Z20200; MUID:99281911; PMID:10355780

A/Accession: T41772

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-292 <KAM>

A/Cross-references: UNIPROT:Q92394; EMBL:L33180; NID:93745835; PIDN:AA63701.1; PID:93745

A/Experimental source: isolate T3

C/Genetics:

A/Note: IAP1

C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 28.0%; Score 109; DB 2; Length 292;
Best Local Similarity 38.3%; Pred. No. 6.5e-05;
Matches 18; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 20 LABAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWYPCCKYL 66
DB 153 IAEAGLFYTGGRGDETVCFDCDCVRDWMHTEDTQGHAAENPQCFYFV 199

RESULT 19

apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus

C/Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30489

R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 253, 17-34, 1999

A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d

A/Reference number: Z20836; MUID:99124785; PMID:9887315

A/Accession: T30489

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-155 <KUZ>

A/Cross-references: UNIPROT:Q9YMI9; EMBL:AF081810; PIDN:AACT0325.1

Query Match 26.0%; Score 101; DB 2; Length 155;
Best Local Similarity 29.2%; Pred. No. 0.00028;
Matches 19; Conservative 13; Mismatches 31; Indels 2; Gaps 1;

QY 4 RIPTFGTW--IYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAHWY 61
DB 7 RLASFNNMSAVDPAAPAEALHAGFYCANRDPFKCAVCHIEIENMISIGSAMSDHGRYSP 66

QY 62 GCKYL 66
DB 67 ACRFV 71

RESULT 20

T37471

apoptosis inhibitor homolog T37F2.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37471, T25380
R;Uren, A.G.
submitted to the EMBL Data Library, January 1997
A;Description: C. elegans IAP homologue.
A;Reference number: Z21708
A;Accession: T37471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-155 <URE>
A;Cross-references: UNIPROT:Q22837; EMBL:U85911; PIDD:AA894330.1
R;Jennard, N.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z20025
A;Accession: T25380
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-155 <WTL>
A;Cross-references: EMBL:Z74045; NID:e1062212; PIDD:CAA98553.1; GSPDB:GN00023; CESP:T27H
C;Genetics:
A;Gene: T27F2.3
A;Map position: 5
A;Intons: 41/3

Query Match 25.7%; Score 100; DB 2; Length 155;
Best Local Similarity 31.9%; Pred. No. 0.00037;
Matches 23; Conservative 12; Mismatches 29; Indels 8; Gaps 3;

Qy 1 YEARIFPGWITV-----SYNKEQLARAGFYALGEGDKYKCFHGGGLTDMKSEDPWE 54
Db 17 YKDLMTFKNFNEYRDPDAKCTSOVAQAGFYCTGP-QSGKCAPCNKEL-DFDEDDPWY 74

Qy 55 QHAKYPCCKYL 66
Db 75 EHTKRDPCFERY 86

RESULT 21
T37474
apoptosis inhibitor homolog C5088.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37474; T20098
R;Uren, A.G.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z21711
A;Accession: T37474
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-308 <URE>
A;Cross-references: UNIPROT:Q18727; EMBL:U72208; PIDD:AA00182.1
R;Percy, C.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19223
A;Accession: T20098
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-308 <WTL>
A;Cross-references: EMBL:Z77654; PIDD:CA801130.1; GSPDB:GN00023; CESP:C5088.2
C;Genetics:
A;Gene: C5088.2
A;Map position: 5
A;Intons: 48/3; 143/1; 191/3

Query Match 24.9%; Score 97; DB 2; Length 308;
Best Local Similarity 30.7%; Pred. No. 0.0016;
Matches 23; Conservative 20; Mismatches 22; Indels 10; Gaps 4;

Qy 1 YEARIFPGWITVSVNK-----EQLARAGFYAL-GSGDK--VKCFHGGGLTDMKSESD 51
Db 17 YKDLMTFKNFNEYRDPDAKCTSOVAQAGFYCTGP-QSGKCAPCNKEL-DFDEDDPWY 74

Db 167 FDRHLPFQNFIPDKRNVKCTSKKLAKAGWISIANKKDXTSAKCPCLVEL-DFDESD 225
Qy 52 PWEQHAKYPCCKYL 66
Db 226 PWEHQHFSASCDFI 240

RESULT 22
T28403
ORF MSV242 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomox
C;Species: Melanoplus sanguinipes entomoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28403
R;Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomoxvirus.
A;Reference number: Z20484; NID:99102612; PMID:9847359
A;Accession: T28403
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-329 <AFO>
A;Cross-references: UNIPROT:Q9YVK0; EMBL:AF063866; NID:g4049647; PIDD:AAC97721.1; PID:g4(
C;Genetics:
A;Note: MSV242

Query Match 22.5%; Score 87.5; DB 2; Length 329;
Best Local Similarity 31.6%; Pred. No. 0.021;
Matches 18; Conservative 10; Mismatches 28; Indels 1; Gaps 1;

Qy 7 TPGTWTIVSVNKEQLARAGFYALGEGDKYKCFHGGGLTDMKSEDPWEQHAKYPCG 63
Db 17 TYDKMNSIETIYWMNAGFTCKGP-SIVECMGRKVLTDWKGDNPFEHITYSKDC 72

RESULT 23
T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43523; T41649; T41700
R;Morishita, J.; Matsusaka, T.; Yanagida, M.
submitted to the EMBL Data Library, August 1999
A;Description: Fission yeast cut17 is required for chromosome segregation.
A;Reference number: Z22536
A;Accession: T43523
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-997 <MOR>
A;Cross-references: UNIPROT:Q14064; EMBL:AB031034; PIDD:BAAB3415.1
R;Harris, D.; Wood, V.; Rajandream, M.A.; Barrett, B.G.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z22007
A;Accession: T41649
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-997 <HAR>
A;Cross-references: EMBL:AL031323; PIDD:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02C
A;Experimental source: strain 97Ch-; cosmid c962
R;Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrett, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z22010
A;Accession: T41700
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 932-997 <MED>
A;Cross-references: EMBL:AL121859; PIDD:CA858376.1; GSPDB:GN00068; SPDB:SPCP31B10.10C
C;Genetics:
A;Gene: cut17; SPCC962.02C; SPDB:SPCP31B10.10C
A;Map position: 3L
A;Intons: 43/3

Query Match 22.5%; Score 87.5; DB 2; Length 997;
Best Local Similarity 30.3%; Pred. No. 0.063;

Matches 23; Conservative 9; Mismatches 33; Indels 11; Gaps 3;

Qy 1 YEAFITFGTIVSYVNK---EQLARAGFY--ALGEG-----DKVCFHGGGLTDMKPS 49
Db 22 YSKRLDTQKKKMPRAKTPETLATVGFYINPISHSNBEKLDNTCTMCTKSPFDMEDD 81

Qy 50 EDPWEQHAQWYPGCKY 65
Db 82 DDPKKEHTHTSPSCPW 97

RESULT 24

C42523

A55R protein - vaccinia virus (strain Copenhagen)

C/Species: vaccinia virus

A/Note: host Homo sapiens (man)

C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004

C/Accession: C42523

R/Johnson, G.P.

submitted to GenBank, June 1990

A/Accession: C42523

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-564 <JOH>

A/Cross-references: UNIPROT:P21073

C/Superfamily: uncharacterized conserved protein with kelch repeats, vaccinia F3L type; F/7-110/Domain: POZ domain homology <POZ>

Query Match 20.4%; Score 79.5; DB 2; Length 564;
Best Local Similarity 24.7%; Pred. No. 0.29;

Matches 19; Conservative 17; Mismatches 22; Indels 19; Gaps 4;

Qy 3 ARITFTGFT---WTYSVNKEQLARAGFYALGEGDKVKCFHGGGLT-----WK 47
Db 313 SKVAIVTCTNSWYIDIPELKYPKSNCGGLADDEYI---YCIIGIRQDSSLTSSIDKMK 369

Qy 48 PSEDPWEQHAQW-YPGC 63
Db 370 PSKRYWQKVAQMRPEKC 386

RESULT 25

JQ1792

SA1P17R protein - vaccinia virus

N/Alternate names: SA1P17R 64.7K protein

C/Species: vaccinia virus

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: JQ1792; C38550

R/Smith, G.L.; Chan, Y.S.; Howard, S.T.

J. Gen. Virol. 72, 1349-1376, 1991

A/Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in

A/Reference number: JQ1767; MUID:91255063; PMID:2045793

A/Accession: JQ1792

A/Molecule type: DNA

A/Residues: 1-564 <SMI>

A/Cross-references: UNIPROT:P24768; DDBJ:D11079; NID:g222717; PIDN:BA01828.1; PID:g2227

A/Experimental source: strain WR

R/Howard, S.T.; Chan, Y.S.; Smith, G.L.

A/Title: Vaccinia virus homologues of the Shope fibroma virus inverted terminal repeat F

A/Reference number: A38550; MUID:91111982; PMID:1846491

A/Accession: C38550

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-564 <HOW>

A/Cross-references: GB:M58052

C/Experimental source: strain WR

C/Superfamily: uncharacterized conserved protein with kelch repeats, vaccinia F3L type; F/7-110/Domain: POZ domain homology <POZ>

Query Match 20.4%; Score 79.5; DB 2; Length 564;
Best Local Similarity 24.7%; Pred. No. 0.29;

Matches 19; Conservative 17; Mismatches 22; Indels 19; Gaps 4;

Qy 3 ARITFTGFT---WTYSVNKEQLARAGFYALGEGDKVKCFHGGGLT-----WK 47
Db 313 SKVAIVTCTNSWYIDIPELKYPKSNCGGLADDEYI---YCIIGIRQDSSLTSSIDKMK 369

Qy 48 PSEDPWEQHAQW-YPGC 63
Db 370 PSKRYWQKVAQMRPEKC 386

RESULT 26

ACFPA2

nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C/Accession: S11679; S10306; S11084

R/Sawruk, B.; Schloos, P.; Betz, H.; Schmitt, B.

EMBO J. 9, 2671-2677, 1990

A/Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel devel

A/Reference number: S11679; MUID:90360975; PMID:1697262

A/Accession: S11679

A/Molecule type: mRNA

A/Residues: 1-576 <SAW>

A/Cross-references: UNIPROT:P17644; EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533

A/Note: 233-ile was also found

R/Baumann, A.; Jonas, P.; Gundelfinger, E.D.

Nucleic Acids Res. 18, 3640, 1990

A/Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acetyl

A/Reference number: S10306; MUID:90301489; PMID:2114015

A/Accession: S10306

A/Molecule type: mRNA

A/Residues: 1-576 <BAU>

A/Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803

R/Jonas, P.; Baumann, A.; Metz, B.; Gundelfinger, E.D.

FEBS Lett. 269, 264-268, 1990

A/Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel n

A/Reference number: S11084; MUID:90353591; PMID:2117557

A/Accession: S11084

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 42-90, 92-576 <JON>

C/Genetics:

A/Gene: FlyBase:ACR-alpha-96Ab

A/Cross-references: FlyBase:FBgn0000039

A/Map position: 3R 96A

A/Intons: 84/3; 136/2; 196/3; 250/1; 445/2; 512/3

C/Superfamily: acetylcholine receptor

C/Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

F/1-41/Domain: signal sequence #status predicted <SIG>

F/42-576/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>

F/43-260/Domain: extracellular #status predicted <EXT>

F/261-287/Domain: transmembrane #status predicted <TM>

F/293-311/Domain: transmembrane #status predicted <TM>

F/327-348/Domain: transmembrane #status predicted <TM>

F/349-326/Domain: intracellular #status predicted <INT>

F/527-545/Domain: transmembrane #status predicted <TM>

F/65,254,570/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/159-183/Diulfide bonds: #status predicted

Query Match 17.0%; Score 66; DB 1; Length 576;
Best Local Similarity 29.0%; Pred. No. 11;
Matches 18; Conservative 10; Mismatches 24; Indels 10; Gaps 2;

Qy 8 FGTWYSVNKEQLARAGFYALGEGDKVKCFHGGGLTDMKPSD-----PWEQHAQWY 61
Db 187 FGSWTYDQGDIDK---HISQKNDKDNKVEIGIDIRBYVPSVEMDILGVARHKKYYP 242

Qy 62 GC 63
Db 243 CC 244

RESULT 27
H72858
apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
C/Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A/Note: dsDNA virus
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: H72858
R/Author: M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Poseee, R.D.
Virology 202, 586-605, 1994
A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A/Reference number: A72850; MUID:94303173; PMID:8030224
A/Accession: H72858
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <A/R>
A/Cross-references: UNIPROT:P41454; GB:L22858; NID:G510708; PIDN:AAA6701.1; PID:G55914C
C/Genetics:
A/Gene: Ac-IAP2

Query Match 16.7%; Score 65; DB 2; Length 249;
Best Local Similarity 32.1%; Pred. No. 5.9;
Matches 17; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

Qy 14 SYNVEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQHAKVPGCKYL 66
Db 103 SVVVDMARRGFYFGAGHLRCSGC-HIVKRYKSVDDAQRHKO---NCKFL 151

RESULT 28
T15907
hypothetical protein E04F6.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15907
R/Author: A.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid E04F6.
A/Reference number: Z18427
A/Accession: T15907
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-444 <PAU>
A/Cross-references: UNIPROT:Q19059; EMBL:U28943; NID:G861333; PID:G861337; PIDN:AAA68358
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:E04F6.6
A/Intons: 41/1; 73/2; 127/2; 173/2; 256/3; 367/3
C/Superfamily: Caenorhabditis elegans hypothetical protein E04F6.6

Query Match 16.7%; Score 65; DB 2; Length 444;
Best Local Similarity 32.8%; Pred. No. 11;
Matches 22; Conservative 4; Mismatches 25; Indels 16; Gaps 4;

Qy 9 GTW-----TYSVNEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQH---AK 58
Db 284 GTMSVKGIPTYPPIWER-----GAIAGRLMNVPPGSGGSDHIGVDRYWSQIQEIGAN 338

Qy 59 WYPGCKY 65
Db 339 WYEG-KY 344

RESULT 29
T15099
hypothetical protein W03F8.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15099
R/Author: D.; Bradshaw, H.; Keppeler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03F8.
A/Reference number: Z18293
A/Accession: T15099

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1808 <JOH>
A/Cross-references: UNIPROT:O44565; EMBL:AF039041; NID:G2736380; PID:G2736388; PIDN:AA594
A/Experimental source: strain Bristol N2; clone W03F8
C/Genetics:
A/Gene: CESP:W03F8.5
A/Map position: 4
A/Intons: 99/2; 255/2; 365/2; 435/3; 565/2; 975/2; 1055/2; 1602/3; 1719/3; 1766/1
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
F:797-842/Domin: laminin-type EGF-like homology <LEG>

Query Match 16.7%; Score 65; DB 2; Length 1808;
Best Local Similarity 25.0%; Pred. No. 43;
Matches 11; Conservative 9; Mismatches 8; Indels 16; Gaps 2;

Qy 32 DKVCFHCGGGLTDMKPSDPM-----EQAKKY 60
Db 74 EQTKCFYC-DSRTWKPRQREPYRLSHRIENVTVTEWDDKRWNY 116

RESULT 30
S12359
nicotinic acetylcholine receptor alpha-1L chain precursor - desert locust
C/Species: Schistocerca gregaria (desert locust)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: S12359
R/Author: J.; Buckingham, S.D.; Shingal, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
EMBO J. 9, 4391-4398, 1990
A/Title: Sequence and functional expression of a single alpha subunit of an insect nicot
A/Reference number: S12359; MUID:91092263; PMID:1702381
A/Accession: S12359
A/Molecule type: mRNA
A/Residues: 1-557 <MAR>
A/Cross-references: UNIPROT:P23414; EMBL:X55439; NID:G10133; PIDN:CAA39081.1; PID:G10134
C/Superfamily: acetylcholine receptor
C/Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F:1-23/Domin: signal sequence #status predicted <SIG>
F:24-557/Product: nicotinic acetylcholine receptor alpha-1L chain #status predicted <MAT>
F:245-266/Domin: transmembrane #status predicted <TM1>
F:274-295/Domin: transmembrane #status predicted <TM2>
F:308-329/Domin: transmembrane #status predicted <TM3>
F:501-523/Domin: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 64.5; DB 2; Length 557;
Best Local Similarity 24.7%; Pred. No. 15;
Matches 18; Conservative 9; Mismatches 13; Indels 33; Gaps 3;

Qy 8 FGTWYSVNEQLARAGFYALGEGDKVCFH-----CGGGLTDMKPSD----- 51
Db 169 FGSMTY-----DGDQIDLKHNQKYDNKKVKGIDLREYPSVEMWDIG 212

Qy 52 -PWEGHAKVPGC 63
Db 213 VPAERHEKTYPC 225

RESULT 31
P00219
RNA-2 polypeptide - arabis mosaic virus (fragment)
N/Contains: coat protein
C/Species: arabis mosaic virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: P00219; P00220
R/Bertoli, D.J.; Harris, R.D.; Edwards, M.L.; Cooper, J.I.; Hawes, W.S.
J. Gen. Virol. 72, 1801-1809, 1991
A/Title: Transgenic plants and insect cells expressing the coat protein of arabis mosaic
A/Reference number: P00219; MUID:91341466; PMID:1875193
A/Accession: P00219
A/Molecule type: genomic RNA
A/Residues: 1-737 <BER>
A/Cross-references: UNIPROT:Q65028; GB:D10086; NID:G221017; PIDN:BA00982.1; PID:d100145C

A:Experimental source: strain 11lac
A:Accession: PQ0220
A:Molecule type: Protein
A:Residues: 233-252 <BE2>
C:Genetics:
A:Map position: segment RNA-2
C:Keywords: polyprotein
F:233-737/Product: coat protein #status experimental <COA>

Query Match 16.6%; Score 64.5; DB 2; Length 737;
Best Local Similarity 32.3%; Pred. No. 20;
Matches 20; Conservative 7; Mismatches 20; Indels 15; Gaps 4;

Qy 12 IYSVVKQQLARAGFYALGEGDKVK-----CFHCGGGL-----TDWKPSDEPWEQHAKYYP 61
Db 447 VYNNFNTLLS-----YLLGIGGVKGVKVKHICSPCTGIVLRVYSEKNGVTNNMNLQFK-YF 501

Qy 62 GC 63
Db 502 GC 503

RESULT 32

coat protein - arabis mosaic virus (fragment)

C:Species: arabis mosaic virus

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C:Accession: S13720; S77995

R:Steinmuller, H.; Himmler, G.; Maltanovich, D.; Kattlinger, H.

Nucleic Acids Res. 18, 7182, 1990

A:Title: Nucleotide sequence of AMV-capsid protein-gene.

A:Reference number: S13720; MUID:91088343; PMID:2263501

A:Accession: S13720

A:Molecule type: genomic RNA

A:Residues: 1-506 <STE>

A:Cross-references: UNIPROT:P24819; EMBL:X55460

A:Accession: S77995

A:Molecule type: protein

A:Residues: 2-21 <HIM>

C:Keywords: polyprotein

F:2-506/Product: coat protein #status predicted <COA>

Query Match 16.3%; Score 63.5; DB 2; Length 506;
Best Local Similarity 32.3%; Pred. No. 18;
Matches 20; Conservative 7; Mismatches 20; Indels 15; Gaps 4;

Qy 12 IYSVVKQQLARAGFYALGEGDKVK-----CFHCGGGL-----TDWKPSDEPWEQHAKYYP 61
Db 216 VYNNFNTLLS-----YLLGIGGVKGVKVKHICSPCTGIVLRVYSEKNGVTNNMNLQFK-YF 270

Qy 62 GC 63
Db 271 GC 272

RESULT 33

hyposethetical protein SPBC19P5.05C SPBC25D12.01C - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39823; T39989

R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrall, B.G.; Boche, G.; Pohl, T.

submitted to the EMBL Data Library, April 1998

A:Reference number: Z21882

A:Accession: T39823

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-607 <LVN>

A:Cross-references: UNIPROT:O60164; EMBL:AL022599; PIDN:CA11653.1; GSPDB:GN00067; SPDB:

A:Experimental source: strain 972h-; cosmid c19P5

R:Lyne, M.; Rajandream, M.A.; Barrall, B.G.; Whithead, S.; Chillingworth, T.; Churcher,

submitted to the EMBL Data Library, July 1998

A:Reference number: Z21897

A:Accession: T39989
A:Molecule type: DNA
A:Residues: 1-454 <LY2>
A:Cross-references: EMBL:AL031158; PIDN:CA20097.1; GSPDB:GN00067; SPDB:SPBC25D12.01C
A:Experimental source: strain 972h-; cosmid c25D12
C:Genetics:
A:Gene: SPBC19P5.05C; SPBC25D12.01C
A:Map position: 2
A:introns: 8/1; 64/1

Query Match 16.3%; Score 63.5; DB 2; Length 607;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 14; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 1 YEAFIFFTGWIY-SVNKEQLARAGFYALG 29
Db 413 YEGRIYIQPWVYDSINKGILERTDLYACG 442

RESULT 34

T30427

probable apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus

C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMPV

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30427

R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 253, 17-34, 1999

A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d

A:Reference number: Z20836; MUID:99124785; PMID:9887315

A:Accession: T30427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-234 <KUZ>

A:Cross-references: UNIPROT:Q9YMP8; EMBL:AF081810; PIDN:AACT0265.1

Query Match 16.2%; Score 63; DB 2; Length 234;
Best Local Similarity 25.4%; Pred. No. 9.4;
Matches 16; Conservative 10; Mismatches 37; Indels 0; Gaps 0;

Qy 4 RIFPFQWITSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKYYPGC 63
Db 90 RAFAAGCGKYGSDANALAACGFFYNGRCREAGCSCGMVVVXKLQRGDDLVIHGVSPRC 149

Qy 64 KYL 66
Db 150 APV 152

RESULT 35

S39502

vegetative storage protein wind 5 - western balsam poplar x cottonwood (fragment)

C:Species: Populus trichocarpa x Populus deltoides (western balsam poplar x cottonwood)

C:Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: S39502

R:David, J.M.; Egeltkrou, B.E.; Coleman, G.D.; Chen, T.H.H.; Haisig, B.E.; Rlemenachneic

Plant Mol. Biol. 23, 135-143, 1993

A:Title: A family of wound-induced genes in Populus shares common features with genes enc

A:Reference number: S39502; MUID:94033285; PMID:8106009

A:Accession: S39502

A:Molecule type: mRNA

A:Residues: 1-324 <DAV>

A:Cross-references: UNIPROT:Q41097; EMBL:L20233; NID:G309838; PID:G309839

Query Match 16.1%; Score 62.5; DB 2; Length 324;
Best Local Similarity 39.6%; Pred. No. 15;
Matches 19; Conservative 2; Mismatches 20; Indels 7; Gaps 2;

Qy 8 FGTWITSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPWEQHAKYYP 53
Db 158 FGEFNTFVNGENLLASVDY-----DKYKLFKSHSPQDVWPFSTISW 200

RESULT 36

A32751
spectact receptor precursor - sea urchin (Strongylocentrotus purpuratus)
C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C/Accession: A32751; PMID:89184581; PMID:2538832
Proc.Natl.Acad.Sci.U.S.A. 86, 2128-2132, 1989
R.Dangott, L.J. Jordan, J.E. Bellef, R.A. Gathers, D.L.
A/Title: Cloning of the mRNA for the protein that crosslinks to the egg peptide spectact.
A/Reference number: A32751; PMID:89184581; PMID:2538832
A/Accession: A32751
A/Molecule type: mRNA
A/Residues: 1-352; 'G', 354-532 <DA2>
A/Cross-references: UNIPROT:P16264; GB:J04518
A/Note: the authors translated the codon CAC for residue 353 as Gly
A/Note: part of this sequence was confirmed by protein sequencing
C/Keywords: membrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-532/Product: spectact receptor #status predicted <MAT>
F:40-144/Domain: scavenger receptor cysteine-rich domain homology <SRC1>
F:150-257/Domain: scavenger receptor cysteine-rich domain homology <SRC2>
F:261-366/Domain: scavenger receptor cysteine-rich domain homology <SRC3>
F:379-485/Domain: scavenger receptor cysteine-rich domain homology <SRC4>

Query Match 16.1%; Score 62.5; DB 2; Length 532;
Best Local Similarity 25.4%; Pred. No. 24;
Matches 17; Conservative 12; Mismatches 17; Indels 21; Gaps 4;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDKVK-CFHCGGGLTDWKPSDDPWEQNAKWP 59
DB 98 FGAHVTF--WVYKGN-----CLGNETRLBEDCYH-----RPGRPALGNAGW 137

QY 60 YPGCKYL 66
DB 138 AAGVECL 144

RESULT 37
T41814
IAP2 orf71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C/Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A/Variety: isolate T3
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41814
R.Gomi, S. Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A/Reference number: 222020; MUID:99281911; PMID:10355780
A/Accession: T41814
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-249 <KAM>
A/Cross-references: UNIPROT:O92435; EMBL:L33180; PIDD:AA63743.1
A/Experimental source: isolate T3
C/Genetics:
A/Note: iap2

Query Match 15.9%; Score 62; DB 2; Length 249;
Best Local Similarity 30.2%; Pred. No. 13;
Matches 16; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

QY 14 SVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQNAKWP 66
DB 103 SVVVDMLARKGFYFGAGHLRCGCG-HIVFKYSVDDAQRHKQ--NCKPV 151

RESULT 38
S28419
lamin B-3 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: S28419
R.Furukawa, K.; Holta, Y.
EMBO J. 12, 97-106, 1993

A/Title: cDNA cloning of a germ cell specific lamin B(3) from mouse spermatocytes and an
A/Reference number: S28419; MUID:93154351; PMID:8094052
A/Accession: S28419
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-474 <RUR>
A/Cross-references: UNIPROT:P48680; EMBL:D13455; NID:9220471; PIDD:BAA02708.1; PIDD:922047;
C/Superfamily: cytoskeletal keratin

Query Match 15.9%; Score 62; DB 2; Length 474;
Best Local Similarity 35.1%; Pred. No. 25;
Matches 13; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 26 YALGEGDKVKCFHCGGGLTDWKPSDDPWEQNAKWP 62
DB 375 YVLRAGQTVVMAAGAGATHSPSTLVWKSQTWVG 411

RESULT 39
B48315
lamin B2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: B48315; S08264; A41068; A56583; S21609
R.Hoeger, T.H.; Zatloukal, K.; Walzenegger, I.; Krohne, G.
Chromosome 99, 379-390, 1990
A/Title: Characterization of a second highly conserved B-type lamin present in cells pre
A/Reference number: A48315; MUID:91106216; PMID:2102682
A/Accession: B48315
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-592 <HOB>
A/Cross-references: UNIPROT:P21619; EMBL:X54098; NID:952866; PIDD:CMA38032.1; PIDD:952867
A/Note: the figure legends for Fig. 5 (African clawed frog) and Fig. 6 (mouse) appear to
sequences in Genbank
R.Hoeger, T.H.; Zatloukal, K.; Walzenegger, I.; Krohne, G.
Chromosome 100, 67-69, 1990
A/Reference number: A56583; MUID:91339548; PMID:2102440
A/Contents: annotation; extratum
A/Note: corrects transposition of Figs. 5 and 6
R.Weber, K.; Plesmann, U.; Traub, P.
FEBS Lett. 261, 361-364, 1990
A/Title: Protein chemical analysis of purified murine lamin B identifies two distinct po
A/Reference number: S08264; MUID:90184461; PMID:2311764
A/Accession: S08264
A/Status: preliminary
A/Status: preliminary
A/Molecule type: protein
A/Residues: 182-206;234-286;290-313; 'R', 315-317; 'X', 319;364-401;466-479; 'X', 481-492 <WEB>
R.Kasahara, K.; Chida, K.; Tsunenaga, M.; Kohno, Y.; Ikuta, T.; Kuroki, T.
J. Biol. Chem. 266, 20018-20023, 1991
A/Title: Identification of lamin B-2 as a substrate of protein kinase C in BALB/MK-2 mou
A/Reference number: A41068; MUID:92041823; PMID:1939065
A/Accession: A41068
A/Molecule type: protein
A/Residues: 165-166; 'X', 169; 'X', 170-172;254-258; 'X', 260-262;478-479; 'X', 481-483; 'X', 485-4
C/Superfamily: cytoskeletal keratin
C/Keywords: nucleus

Query Match 15.9%; Score 62; DB 2; Length 592;
Best Local Similarity 35.1%; Pred. No. 31;
Matches 13; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 26 YALGEGDKVKCFHCGGGLTDWKPSDDPWEQNAKWP 62
DB 493 YVLRAGQTVVMAAGAGATHSPSTLVWKSQTWVG 529

RESULT 40
T43634
nicotinic acetylcholine receptor alpha chain - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43634

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OM protein - protein search, using SW model

Run on: June 15, 2005, 17:39:48 ; Search time 108.5 Seconds
(without alignments)
233.180 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIPTFTGWTIVSVNKEQL.....KPSHPDWECHAKWPGCKYL 66

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Gapop 10.0 , Gapext 0.5

Searched: 1710399 seges, 38333425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
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- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	389	100.0	66 9 US-09-201-936-25	Sequence 25, Appl
2	389	100.0	66 16 US-10-600-272-25	Sequence 25, Appl
3	389	100.0	107 9 US-09-965-967-20	Sequence 20, Appl
4	389	100.0	236 13 US-10-024-433-4	Sequence 4, Appl
5	389	100.0	278 9 US-09-964-859-39	Sequence 39, Appl
6	389	100.0	497 9 US-09-974-592-4	Sequence 4, Appl
7	389	100.0	497 9 US-09-201-936-4	Sequence 4, Appl
8	389	100.0	497 15 US-10-366-307-2	Sequence 2, Appl
9	389	100.0	497 16 US-10-636-065-219	Sequence 219, Appl
10	389	100.0	497 16 US-10-600-272-4	Sequence 4, Appl
11	366	94.1	66 9 US-09-201-936-24	Sequence 24, Appl

12	366	94.1	66 16 US-10-600-272-24	Sequence 24, Appl
13	366	94.1	496 9 US-09-974-592-10	Sequence 10, Appl
14	366	94.1	496 9 US-09-201-936-10	Sequence 10, Appl
15	366	94.1	496 16 US-10-636-065-225	Sequence 225, Appl
16	366	94.1	496 16 US-10-600-272-10	Sequence 10, Appl
17	352	90.5	496 16 US-10-482-952-5	Sequence 5, Appl
18	347	89.2	236 13 US-10-024-433-2	Sequence 2, Appl
19	347	89.2	464 15 US-10-343-115-2	Sequence 2, Appl
20	249	64.0	50 14 US-10-138-618-28	Sequence 28, Appl
21	249	64.0	50 14 US-10-138-618-29	Sequence 29, Appl
22	249	64.0	50 14 US-10-138-618-32	Sequence 32, Appl
23	211	54.2	68 9 US-09-201-936-26	Sequence 26, Appl
24	211	54.2	68 16 US-10-600-272-26	Sequence 26, Appl
25	211	54.2	557 16 US-10-482-952-9	Sequence 9, Appl
26	211	54.2	604 9 US-09-974-592-6	Sequence 6, Appl
27	211	54.2	604 9 US-09-201-936-6	Sequence 6, Appl
28	211	54.2	604 14 US-10-232-286-4	Sequence 4, Appl
29	211	54.2	604 14 US-10-141-618-6	Sequence 6, Appl
30	211	54.2	604 15 US-10-366-307-6	Sequence 6, Appl
31	211	54.2	604 16 US-10-636-065-221	Sequence 221, Appl
32	211	54.2	604 16 US-10-600-272-6	Sequence 6, Appl
33	211	54.2	604 16 US-10-730-476A-79	Sequence 79, Appl
34	211	54.2	604 16 US-10-825-282-40	Sequence 40, Appl
35	211	54.2	604 17 US-10-934-717-4	Sequence 4, Appl
36	211	54.2	1140 14 US-10-353-461-8	Sequence 8, Appl
37	205	52.7	68 9 US-09-201-936-28	Sequence 28, Appl
38	205	52.7	68 14 US-10-041-859-18	Sequence 18, Appl
39	205	52.7	68 16 US-10-600-272-28	Sequence 28, Appl
40	205	52.7	172 14 US-10-041-859-12	Sequence 12, Appl
41	205	52.7	268 14 US-10-323-643-10	Sequence 10, Appl
42	203	52.2	600 9 US-09-974-592-12	Sequence 12, Appl
43	203	52.2	600 16 US-10-482-952-1	Sequence 1, Appl
44	199	51.2	68 14 US-10-041-859-14	Sequence 14, Appl
45	199	51.2	172 14 US-10-041-859-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-25
Sequence 25, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201, 936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011, 356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576, 956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511, 485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2
US-10-600-272-25
; Sequence 25, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT FILING DATE: US/10/600,272
; PRIOR APPLICATION NUMBER: 2003-06-20
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/1B96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-272-25

Query Match 100.0%; Score 389; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Qy 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3
US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 60
Db 15 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPWEQHAKEY 74
Qy 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 4
US-10-024-433-4
; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT FILING DATE: US/10/024,433
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-4

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Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 5
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

Query Match 100.0%; Score 389; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;


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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PGCKYL 66
Db 106 PGCKYL 111

RESULT 6
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Teang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIR FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 7
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
```

```
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQHAKWY 60
Db 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 8
US-10-366-307-2
; Sequence 2, Application US/10366307
; Publication No. US20030224399A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Determining the Prognosis
; TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
; FILE REFERENCE: P-LJ 5659
; CURRENT APPLICATION NUMBER: US/10/366,307
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-307-2

Query Match 100.0%; Score 389; DB 15; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQHAKWY 60
Db 265 YEARIFFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMWQHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 9
US-10-636-065-219
; Sequence 219, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
```

```

PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 219
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-10-636-065-219

```

Query Match	100.0%;	Score 389;	DB 16;	Length 497;
Best Local Similarity	100.0%;	Pred. No. 2.6e-38;		
Matches	66;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

Qy 1 YEARI FTFGW IYSVNKEQLARAGFALGEGDKVKCKCHGGGLTDWKSEDPMEQHAKMY 60
Db 265 YEARI FTFGW IYSVNKEQLARAGFYALGEGDKVKKCHCGGGLTDWKSEDPMEQHAKMY 324

QY	61	PGCKYL	66
Db	325	PGCKYL	330

```

RESULT 10
US-10-600-272-4
; Sequence 4, Application US/10600272
; Publication No. US200400157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneljuk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; FILE REFERENCE: 079821/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/010322
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: SeqSIO for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-600-272-4

```

Query Match	100.0%;	Score 389;	DB 16;	Length 497;
Best Local Similarity	100.0%;	Pred. No. 2.6e-38;		
Matches 66;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy 1 YEARIPTFGTWIYSVNKEQLARAGFALGEGDKVKCFHCGGGITDWMKPSSEDPMEQHAKMY 60
Dd 265 YEARIPTFGTWIYSVNKEQLARAGFALGEGDKVKCFHCGGGITDWMKPSSEDPMEQHAKMY 324

QY	61	PGCKYL	66
Db	325	PGCKYL	330

```

RESULT 11
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

```

```

? APPLICANT: listcom, petec
? TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
? TITLE OF INVENTION: PROBS. AND DETECTION METHODS
? FILE REFERENCE: 07891/003003
? CURRENT APPLICATION NUMBER: US/09/201,936
? EARLIER FILING DATE: 1998-12-01
? EARLIER APPLICATION NUMBER: 09/011,356
? EARLIER FILING DATE: 1998-02-04
? EARLIER APPLICATION NUMBER: PCT/IB96/01022
? EARLIER FILING DATE: 1996-08-05
? EARLIER APPLICATION NUMBER: 08/576,956
? EARLIER FILING DATE: 1995-12-22
? EARLIER APPLICATION NUMBER: 08/511,485
? EARLIER FILING DATE: 1995-08-04
? NUMBER OF SEQ ID NOS: 45
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 24
? LENGTH: 66
? TYPE: PRT
? ORGANISM: Mus musculus
? US-09-201-936-24

```

Query Match	94.1%	Score 366;	DB 9;	Length 66;
Best Local Similarity	95.5%;	Pred. No. 1.9e-36;		
Matches 63; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Oy

1 YEARLFTPGTWIYSVNKEQLRAGFYALGEGDYKCFHCOCGGGLTDWKPSEDPMWEQNAKMV 600
				:				

D8

1 YEARIVTFGTWTISYVNKEQLRAGFYALGEGDYKCFHCOCGGGLTDWKPSDDPMDQNAKCY 600

Qy	61	PGCKYL	66
Db	61	PGCKYL	66

```

RESULT 12
US-10-600-272-24
Sequence 24, Application US/10600272
Publication NO. US20040057232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003006
CURRENT APPLICATION NUMBER: US/10/600,272
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: PCT/IB96/01022
PRIOR FILING DATE: 1996-08-05
PRIOR APPLICATION NUMBER: US 08/576,956
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: US 08/511,485
PRIOR FILING DATE: 1993-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 66
TYPE: PRT
ORGANISM: Mus musculus
US-10-600-272-24

```

Query Match	94.1%;	Score 366;	DB 16;	Length 66;
Best Local Similarity	95.5%;	Pred. No. 1.9e-36;		
Matches 63; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 YEARI FTFGW IYSVNKEQLARAGFALGEGDKVKCFHCGGGLTDWKSSEDPMEDHAKMY 60
|||||
Db 1 YEARI VTFGW IYSVNKEQLARAGFALGEGDKVKCFHCGGGLTDWKSSEDPMWDHAKCY 60
|||||

Query Match	94.1%;	Score 366;	DB 9;	length 496;
Best Local Similarity	95.5%;	Pred. No. 1.6e-35;		
Matches 63; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

1 YEARIFTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDEPWEQHAQMY 60

Db 264 YEARI VTFGTWYISVNKEOLARAGFYALGEGDKYKCFHCGGGLTDMKPSBEDPWDOHAKCY 32

DB 264 YEARIIVIPGIMLYSVNKEQIARAGFYALSGDKVCFHC3GGTIDWKPSBDPMQHAACY 32

QY	61	PGCKYL	66
nb	334	PGCKYR	336

Db 324 PGCKYL 329

RESULT 15

US-10-636-065-225
Sequence 225. Application US/10636065

Sequence 225, Application US/10636065
Publication No. US20040127694A1
CENTRAL INFORMATION

```

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.

```

APPLICANT: Baired, Stephen

APPLICANT: Bairstow, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean

APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

FILE REFERENCE: 07891

FILE REFERENCE: 01891/023003
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07

;
 ; CURRENT FILING DATE: 2003-08-07
 ;
 ; PRIOR APPLICATION NUMBER: 09/672,717
 ;
 ; PRIOR FILING DATE: 2000-08-28
 ;

```

; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225

```

```

: SEQ ID NO 223
:
: LENGTH: 496
:
: TYPE: PRT

```

```

;      TYPE: PRT
;
;      ORGANISM: Mus musculus
;
;      MS-10-636-065-225

```

US-10-636-065-225

Query Match	94.1%;	Score 366;	DB 16;	Length 496;
Best Local Similarity	95.5%;	Pred. No. 1.6e-35;		

Base local similarity 95.3%; Freq. NO. 1.0e-35;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 YEAR1PTFGT1Y1SVNKEOLARAGFVALGEGNKVKCFHCGGG1TDWTPSEDDPWEBOHAKMY 60

264 Y E A R I T F G T I Y S V N K E Q L R A G F Y A L G E G D K V K C H C G G L T D W K R S E D W D Q H A K C Y 323

61 PGCKYL 66

cy	61	PGCKYL	66
hb	324	PGCKYL	329

Db 324 PGCKYL 329

RESULT 16

US-10-600-272-10
Sequence 10, Application US/10600272

GENERAL INFORMATION:
; Publication No. US20040157232A1
; Sequence ID, Application US/106002/12

```

; GENERAL INFORMATION:
; APPLICANT: Kornejuk, Robert G.
; AGENCY: MacKenzie Alexander P

```

```

; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

```

INVENTOR: LISTON, PETER
TITLE OF INVENTION: MAMMALIAN TAD GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003006

FILE REFERENCE: 07891/003006
CURRENT APPLICATION NUMBER: US/10/600,272
CURRENT FILING DATE: 2002-05-20

; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/011,356

PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: PCT/IB96/01022

PRIOR FILING DATE: 1996-08-05

```

; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-600-272-10

Query Match
Best Local Similarity 94.1%; Score 366; DB 16; Length 496;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 60
DB 264 YEARIVTFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 17
US-10-482-952-5
; Sequence 5, Application US/10482952
; Publication No. US20040254136A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York, et al.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND RELATED METHODS FOR REGULATING CEL
; FILE REFERENCE: 0575/64078-A-PCT/JPW/ANX
; CURRENT APPLICATION NUMBER: US/10/482,952
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 496
; TYPE: PRT
; ORGANISM: human
US-10-482-952-5

Query Match
Best Local Similarity 90.5%; Score 352; DB 16; Length 496;
Matches 61; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 60
DB 264 YEARIVTFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 18
US-10-024-433-2
; Sequence 2, Application US/10024433
; Publication No. US20020086409A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 236
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-433-2

Query Match
Best Local Similarity 89.2%; Score 347; DB 13; Length 236;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 60
DB 4 YEARIVTFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 19
US-10-343-115-2
; Sequence 2, Application US/10343115
; Publication No. US20040072999A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: Novel inhibitor of apoptosis protein
; FILE REFERENCE: IAPL-7BHM5
; CURRENT APPLICATION NUMBER: US/10/343,115
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-115-2

Query Match
Best Local Similarity 89.2%; Score 347; DB 15; Length 464;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARIFPGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 60
DB 232 YEARIVTFGTWISVNVKEQLARAGFYALGEGDKVCKFCGCGGLTDMKPSDPMWEOHAKMY 291
QY 61 PGCKYL 66
DB 292 PGCKYL 297

RESULT 20
US-10-138-618-28
; Sequence 28, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 40

RESULT 21
US-10-138-618-29
Sequence 29, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 40

RESULT 22
US-10-138-618-32
Sequence 32, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQAHAKVYPGCKYL 40

RESULT 23
US-09-201-936-26
Sequence 26, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.


```

Db      255 HAARKTEFFNPSSVLVNPBQLASGFYVNGSDVKCFCCDGGJRCWESGDDPWNQHAAX 314
Oy      59 WYPGCKYL 66
        ||:|||
Db      315 WFPRCXYL 322

RESULT 27
US-09-201-936-6
; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-6

Query Match          54.2%; Score 211; DB 9; Length 604;
Best Local Similarity 57.4%; Pred. No. 1,le-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 14;

Oy      1 YEAR1FTGTGWYS--VNKEQLARAGFYALGSGDKVKCFHCGGSLTMDKPSDSDPWEOHAX 58
        |||||
Db      255 HAARKTEFFNPSSVLVNPBQLASGFYVNGSDVKCFCCDGGJRCWESGDDPWNQHAAX 314
        |||||
Oy      59 WYPGCKYL 66
        ||:|||
Db      315 WFPRCXYL 322

RESULT 28
US-10-232-286-4
; Sequence 4, Application US/10232286
; Publication No. US20030143579A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSES: FLHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,286

```

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1      FILING DATE: 30-Aug-2002
2      CLASSIFICATION: <Unknown>
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US/08/569,749
5      FILING DATE: <Unknown>
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Brezner, David J.
8      REGISTRATION NUMBER: 24,774
9      REFERENCE/DOCKET NUMBER: A-62464/DJB
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: (415)781-1989
12     TELEFAX: (415)398-3249
13     INFORMATION FOR SEQ ID NO: 4:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 604 amino acids
16     TYPE: amino acid
17     STRANDEDNESS: single
18     TOPOLOGY: linear
19     MOLECULAR TYPE: protein
20     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
21     US-10-232-286-4
22
23     Query Match      54.2%; Score 211; DB 14; Length 604;
24     Best Local Similarity 57.4%; Pred. No. 1,1e-16;
25     Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
26
27     QY      1 YEARIFPGWTIVS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMWEGHAK 58
28           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
29     DB      255 HAAFKFTFFWNPSSVLVNPBQLASAGFYVGNNSDVACFCDDGGLRCMESGDDPMVQHAK 314
30           ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
31
32     QY      59 WYPCCKYL 66
33           ||:|:|:|:|
34     DB      315 WFPRCGYL 322
35
36 RESULT 29
37 US-10-141-618-6
38 ; Sequence 6, Application US/10141618
39 ; Publication No. US20030165887A1
40 ; GENERAL INFORMATION:
41 ; APPLICANT: Reed, John C.
42 ; TITLE OR INVENTION: Methods For Determining the Prognosis
43 ; FOR CANCER PATIENTS USING TUCAN
44 ; FILE REFERENCE: P-LJ 5254
45 ; CURRENT APPLICATION NUMBER: US/10/141,618
46 ; CURRENT FILING DATE: 2002-05-07
47 ; PRIOR APPLICATION NUMBER: US 60/289,233
48 ; PRIOR FILING DATE: 2001-05-07
49 ; PRIOR APPLICATION NUMBER: US 60/356,934
50 ; PRIOR FILING DATE: 2002-02-12
51 ; PRIOR APPLICATION NUMBER: US 09/388,221
52 ; PRIOR FILING DATE: 1999-09-01
53 ; NUMBER OF SEQ ID NOS: 15
54 ; SOFTWARE: FastSeq for Windows Version 4.0
55 ; SEQ ID NO 6
56 ; LENGTH: 604
57 ; TYPE: PRT
58 ; ORGANISM: Homo sapiens
59 US-10-141-618-6
60
61     Query Match      54.2%; Score 211; DB 14; Length 604;
62     Best Local Similarity 57.4%; Pred. No. 1,1e-16;
63     Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
64
65     QY      1 YEARIFPGWTIVS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSBDPMWEGHAK 58
66           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67     DB      255 HAAFKFTFFWNPSSVLVNPBQLASAGFYVGNNSDVACFCDDGGLRCMESGDDPMVQHAK 314
68           ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
69
70     QY      59 WYPCCKYL 66
71           ||:|:|:|:|
72     DB      315 WFPRCGYL 322

```



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RESULT 34
US-10-825-282-40
; Sequence 40, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-40
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Query Match 54.2%; Score 211; DB 16; Length 604;
Best Local Similarity 57.4%; Pred. No. 1.1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
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```
Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKPSDDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322
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RESULT 35
US-10-934-717-4
; Sequence 4, Application US/10934717
; Publication No. US20050037416A1
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/934,717
; FILING DATE: 03-Sep-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/332,286
; FILING DATE: 30-Aug-2002
; APPLICATION NUMBER: US/08/569,749
; FILING DATE: <Unknown>
```

```
ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-934-717-4
```

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Query Match 54.2%; Score 211; DB 17; Length 604;
Best Local Similarity 57.4%; Pred. No. 1.1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
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Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKPSDDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322
```

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RESULT 36
US-10-353-461-8
; Sequence 8, Application US/10353461
; Publication No. US20030176682A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; TITLE OF INVENTION: Molecular characterisation of chromosome translocation
; TITLE OF INVENTION: c(11;18) (q21;q21) and its correlation to
; FILE REFERENCE: PMA/MALT/V043
; CURRENT APPLICATION NUMBER: US/10/353,461
; CURRENT FILING DATE: 2003-01-26
; PRIOR APPLICATION NUMBER: US/09/579,692
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/138,834
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-461-8
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Query Match 54.2%; Score 211; DB 14; Length 1140;
Best Local Similarity 57.4%; Pred. No. 2.1e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
```

```
Qy 1 YEARITFGTWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTDMKPSDDPWEOHAK 58
Db 255 HAARFKTFPWPSSVLVNPBQLASAGFYVGNSDVXCFCCDGLRCWESGDDPWVOHAK 314
Qy 59 WYPCCKYL 66
Db 315 WFPRCRYL 322
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RESULT 37
US-09-201-936-28
; Sequence 28, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Kornelink, Robert G.
```

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; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-09-201-936-28

```

```

Query Match          52.7%; Score 205; DB 9; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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Qy 3 AR1FTFGTWIYSVVK--EQ1ARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPMEQHAKMY 60
Db 3 AR1RTFAEMWRGKQRPBELAEAGFFYTGQGDTRCFCDDGGLKDWEPDAPWQOHAKMY 62

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Qy 61 PGCKYL 66
Db 63 DRCEYV 68

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RESULT 38
US-10-041-859-18
; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-041-859-18

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```

Query Match          52.7%; Score 205; DB 14; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

```

```

Qy 3 AR1FTFGTWIYSVVK--EQ1ARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPMEQHAKMY 60
Db 3 AR1RTFAEMWRGKQRPBELAEAGFFYTGQGDTRCFCDDGGLKDWEPDAPWQOHAKMY 62
Qy 61 PGCKYL 66
Db 63 DRCEYV 68

```

```

RESULT 39
US-10-600-272-28
; Sequence 28, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-600-272-28

```

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Query Match          52.7%; Score 205; DB 16; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.6e-17;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

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```

Qy 3 AR1FTFGTWIYSVVK--EQ1ARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPMEQHAKMY 60
Db 3 AR1RTFAEMWRGKQRPBELAEAGFFYTGQGDTRCFCDDGGLKDWEPDAPWQOHAKMY 62

```

```

Qy 61 PGCKYL 66
Db 63 DRCEYV 68

```

```

RESULT 40
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryzja pseudotsugata
US-10-041-859-12

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Query Match          52.7%; Score 205; DB 14; Length 172;
Best Local Similarity 50.0%; Pred. No. 1.5e-16;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

```

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Qy 3 AR1FTFGTWIYSVVK--EQ1ARAGFYALGEGDKVCKFCGCGGLTDMKPSDDPMEQHAKMY 60

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Db	70	ARLRTFAWPRGLKQRPBELABAGFFYTGOBDKTRCFCCDGLKDWEPDAPWOOHAWY	129
Oy	61	PGCKYL	66
Db	130	DRCEYV	135

Search completed: June 15, 2005, 17:58:16
Job time : 108.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 15, 2005, 17:19:12 ; Search time 112.5 Seconds
(without alignments)
300.420 Million cell updates/sec

Title: US-10-600-272-25

Perfect score: 389
Sequence: 1 YEARIPTFTGTWYSVNKEQL.....KPSEDPWEQHAKEYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprotc:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	100.0	497	1	BIR4_HUMAN
2	377	96.9	496	1	BIR4_RAT
3	377	96.9	496	2	Q9E0F0
4	377	96.9	501	2	Q9E0C4
5	372	95.6	501	2	Q9E0D5
6	368	94.6	496	1	BIR4_MOUSE
7	347	89.2	236	1	BIR8_HUMAN
8	347	89.2	236	2	Q6PIA0
9	347	89.2	236	2	Q6IPY1
10	341	87.7	236	1	BIR8_PANTR
11	338	86.9	236	1	BIR8_GORGO
12	322	82.8	106	2	Q9E0R6
13	287	73.8	493	2	Q9UVR8
14	255	65.6	109	2	Q8WNY4
15	219	56.3	280	2	Q6TVV9
16	216	55.5	322	2	Q6DBV7
17	216	55.5	405	2	Q6UWH2
18	216	55.5	415	2	Q7SXU1
19	211	54.2	287	2	Q6E7G7
20	211	54.2	604	1	BIR3_HUMAN
21	209	53.7	358	1	PIAP_PIG
22	206	53.0	602	2	Q9E0E5
23	205	52.7	268	1	IAP3_NPVOP
24	204	52.4	195	2	Q9IA70
25	204	52.4	197	2	Q9IA69
26	204	52.4	611	1	BIR_CHICK
27	203	52.2	269	2	Q6OKJ6
28	203	52.2	374	2	Q92INO
29	203	52.2	600	1	BIR3_MOUSE
30	202	51.9	616	2	Q804E2
31	202	51.9	628	2	Q8UWD2

32	202	51.9	647	2	Q7T0K2
33	202	51.9	654	2	Q6ZM93
34	199	51.2	346	2	Q8IS31
35	199	51.2	346	2	Q968T8
36	198	50.9	589	2	Q9E0E8
37	198	50.9	589	2	Q9OZC6
38	197	50.6	534	2	Q8IZ20
39	197	50.6	589	2	Q6P6S1
40	197	50.6	612	1	BIR2_MOUSE
41	197	50.6	618	1	BIR2_HUMAN
42	196	50.4	283	2	Q8OLK8
43	196	50.4	604	2	Q6DDY3
44	195	50.1	263	2	Q80SP4
45	195	50.1	403	2	Q8WRD9

ALIGNMENTS

RESULT 1
ID BIR4_HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9N014;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP-like protein) (HILP).
DE (IAP-like protein) (HILP).
GN Name=BIRC4; Synonyms=API3, IAP3, XIAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=9619249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Pablicke C., Lefebvre C., Baird S., Chertton-Horvat G., Farahani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."
RL Nature 379:349-353(1996).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Giffillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors."
RL EMBO J. 15:2685-2694(1996).
[3]
RP SEQUENCE FROM N.A.
RC Grafiham D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Pelngold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Shuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E., Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RC STRAIN=Wistar; TISSUE=Ovary;

RC STRAIN=Wistar; TISSUE=Ovary;

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RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL; AF304334; AAC41193.1; -.
DR HSSP; P98170; 1151.
DR GO; GO:0000451; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query March 96.9%; Score 377; DB 2; Length 501;
Best Local Similarity 95.5%; Pred. No. 1.9e-35;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKYKCHCGGLTDMKPSBDPMEQHAKMY 60
DQ 264 YDARIVTFGTWIVSVNKEQLARAGFYALGEGDVKYKCHCGGLTDMKPSBDPMEQHAKMY 323
QY 61 PGCKYTL 66
DB 324 PGCKYTL 329

RESULT 5
Q9E005 PRELIMINARY; PRT; 501 AA.
AC Q9E005;
DT 01-MAR-2001 (TREMBlrel. 16; Created)
DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24; Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RX MEDLINE=22642584; PubMed=12606402;
RA Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Frlis R.R.,
RA Dharmarajan A.M.;
RT "Regulated expression of inhibitor of apoptosis protein 3 in the rat
RT corpus luteum.";
RL Biol. Reprod. 68:2232-2240(2003).
DR EMBL; AF304333; AAC41192.1; -.
DR HSSP; P98170; 1151.
DR GO; GO:0000451; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 501 AA; 56548 MW; 0973BFB28B81C5A0 CRC64;

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Query March 95.6%; Score 372; DB 2; Length 501;
Best Local Similarity 93.9%; Pred. No. 7.3e-35;
Matches 62; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEQLARAGFYALGEGDVKYKCHCGGLTDMKPSBDPMEQHAKMY 60
DQ 264 YDARIVTFGTWIVSVNKEQLARAGFYALGEGDVKYKCHCGGLTDMKPSBDPMEQHAKMY 323
QY 61 PGCKYTL 66
DB 324 PGCKYTL 329

RESULT 6
BIR4 MOUSE
ID BIR4 MOUSE STANDARD; PRT; 496 AA.
AC Q60959; 008865;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN Name=Birc4; Synonyms=Alpa, Ap13, Miha, Xiap;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farhanli R., Lefebvre C., Korneluk R.G., Mackenzie A.B.;
RX Submitted (JUN-1997) to the EMBL/Genbank/DBJ database.
RL
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSSP; P98170; 1151.
DR MGD; MGI:107572; Birc4.
DR GO; GO:0001719; P:inhibition of caspase activation; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.

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DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Repeat; Zinc-finger.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-type.
FT CONFLICT 208 208 E -> K (in Ref. 2).
FT CONFLICT 317 317 E -> D (in Ref. 2).
FT CONFLICT 322 322 W -> C (in Ref. 2).
FT CONFLICT 346 346 S -> P (in Ref. 2).
FT CONFLICT 360 360 I -> L (in Ref. 2).
FT CONFLICT 388 388 I -> L (in Ref. 2).
FT CONFLICT 449 449 C -> S (in Ref. 2).
FT CONFLICT 462 462 V -> F (in Ref. 2).
FT CONFLICT 468 468 V -> A (in Ref. 2).
FT CONFLICT 490 490 K -> N (in Ref. 2).
SQ SEQUENCE 496 AA; 56079 MW; ECSFAE0799F2CDD8 CRC64;

Query Match 94.6%; Score 368; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2.1e-34;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YEARIFPGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 60
Db 264 YEARIVFGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 323

Qy 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 7
BIR_HUMAN
ID BIR_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN Name-BIRC8; Synonyms=ILP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143; DOI=10.1006/geno.2001.6635;
RX DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Elben L.J., Lewis J., Refey S.B.,
RA Praticenti A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezroni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX.
CC -1- SUBUNIT: Binds to caspase-9.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -1- SIMILARITY: Belongs to the IAP family.

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CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81992.1; -.
DR HSSP; P98170; 1G73.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS01143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger.
FT REPEAT 7 70 BIR.
FT ZN_FING 189 224 RING-type.
FT CONFLICT 196 196 Y -> H (in Ref. 2).
SQ SEQUENCE 236 AA; 27115 MW; CB7F034B0DDPAP9D CRC64;

Query Match 89.2%; Score 347; DB 1; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.0e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIFPGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 60
Db 4 YEARIVFGTWISVYNKEQLARAGFYALGEGDKYKCFHCGGGLTDMKPSBDPMQHAHMY 63

Qy 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 8
OGPIAO
ID OGPIAO PRELIMINARY; PRT; 236 AA.
AC OGPIAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Baculoviral IAP repeat-containing 8.
GN Name-BIRC8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schietz T.E.,
RA Brownstein M.J., Ustin T.B., Tohilyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hailton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC039318; AA039318.1;
DR GO: GO:0000151; C:ubiquitin-protein ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR_1.
DR SMART: SM00238; BIR; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 236 AA; 27077 MW; DP38350311PDAFPR CRC64;

Query Match 89.2%; Score 347; DB 2; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.8e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFGTWIYSVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPEQHAQMY 60
DB 4 YEARLITFGTWIYSVNKEQLARAGFYALGEGDKVCKFCGGLANMKPXEDEPWEQHAQMY 63
QY 61 PGCKYL 66
DB 64 PGCKYL 69

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RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC071665; AA071665.1;
DR GO: GO:0000151; C:ubiquitin-protein ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR_2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 338 AA; 38622 MW; DC17979CFG92E84DF CRC64;

Query Match 89.2%; Score 347; DB 2; Length 338;
Best Local Similarity 84.8%; Pred. No. 4.1e-32;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEARITFGTWIYSVNKEQLARAGFYALGEGDKVCKFCGGLTDMKPSDPEQHAQMY 60
DB 106 YEARLITFGTWIYSVNKEQLARAGFYALGEGDKVCKFCGGLANMKPXEDEPWEQHAQMY 165
QY 61 PGCKYL 66
DB 166 PGCKYL 171

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RESULT 9
Q61PY1 PRELIMINARY; PRT; 338 AA.
ID Q61PY1;
AC Q61PY1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BIRC8 protein.
GN Name=BIRC8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derye J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RESULT 10
BIR8_PANTR STANDARD; PRT; 236 AA.
ID Q5W72;
AC Q5W72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonyms=ILP2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1126/MB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Prattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 1 BIR repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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DR EMBL; AY030052; AAK49776.1; -.
DR HSSP; P98170; 1G73.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT 70 BIR.
FT ZN FING 189 224 RING-type.
SQ SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;

Query Match 87.7%; Score 341; DB 1; Length 236;
Best Local Similarity 83.3%; Pred. No. 1,4e-31;
Matches 55; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEY 60
DB 4 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 11
BIRB_GORGO
ID BIRB_GORGO STANDARD; PRT; 236 AA.
AC G95W71;
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (inhibitor of apoptosis-
like protein 2) (IAP-like protein 2) (ILP-2).
GN Name=BIRC8; Synonyms=ILP2;
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OC NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RX DOI=10.1128/MCB.21.13.4292-4301.2001;
RA Richter B.W.M., Mir S.S., Elden L.J., Lewis J., Reffey S.B.,
RA Fractini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Natarangelo L.D., Vezoni P., Fearhead R.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (by
similarity).
CC -1- SUBUNIT: Binds to caspase-9 (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 1 BIR-repeat.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.

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DR EMBL; AY030053; AAK49777.1; -.
DR HSSP; P98170; 1G73.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT 70 BIR.
FT ZN FING 189 224 RING-type.
SQ SEQUENCE 236 AA; 27120 MW; C3A70E39EB44284C CRC64;

Query Match 86.9%; Score 338; DB 1; Length 236;
Best Local Similarity 81.8%; Pred. No. 3,2e-31;
Matches 54; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEY 60
DB 4 YEARIPTFGTWISVYNKEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEY 63

QY 61 PGCKYL 66
DB 64 PGCKYL 69

RESULT 12
Q96RW6 PRELIMINARY; PRT; 106 AA.
ID Q96RW6
AC Q96RW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE IAP-like protein 3.
GN Name=ILP3;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164681; AAK81891.1; -.
DR HSSP; P98170; 1G73.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 106 AA; 12360 MW; 6BBAD3AE80A891 CRC64;

Query Match 82.8%; Score 322; DB 2; Length 106;
Best Local Similarity 94.6%; Pred. No. 1,1e-29;
Matches 53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 WISYVNEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEYPGCKYL 66
DB 2 WISYVNEQLARAGFYALGSDGVKCFHCGGGLTDMKPSDEPWEQHAKEYPGCKYL 57

RESULT 13
Q8UVF8 PRELIMINARY; PRT; 493 AA.
ID Q8UVF8
AC Q8UVF8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN Name=IAP3;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF451854; AL447170.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 73.8%; Score 287; DB 2; Length 493;
Best Local Similarity 71.2%; Pred. No. 6e-25;
Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMEQHAQVY 60
DB 264 YERRIQFLWIVYVNHLEHLAGFYSTGNDHYVCFHCGGGLQEMKENEDPMDQHAQV 323
QY 61 PGCKYL 66
DB 324 PGCKFL 329

RESULT 14
Q8WMY4 PRELIMINARY; PRT; 109 AA.
ID Q8WMY4
AC Q8WMY4;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN Name=XIAP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AL46179.1; -.
DR HSSP; P98170; 1130.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC98213DBED CRC64;

Query Match 65.6%; Score 255; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 7.1e-22;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMEQHAQVY 48
DB 57 YEARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMEQHAQV 104

RESULT 15
Q6VTY9 PRELIMINARY; PRT; 280 AA.
ID Q6VTY9
AC Q6VTY9;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Choriostoma fumiterana defective nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
NCBI_TaxID=74660;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138;
RA Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.;
RT "Characterization of an overexpressed spindle protein during a
Baculovirus infection."
RL Virology 268:56-67(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY327402; AA091688.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; ProtInh_132_IAP.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 280 AA; 32179 MW; CA8804614BFD1A1 CRC64;

Query Match 56.3%; Score 219; DB 2; Length 280;
Best Local Similarity 54.5%; Pred. No. 2.9e-17;
Matches 36; Conservative 13; Mismatches 15; Indels 2; Gaps 1;

QY 3 ARIFFGTWIVSVNKEOLARAGFYALGEGDKVCFHCGGGLTDMKPSDPMEQHAQVY 60
DB 115 ARLKTFVDPVPSIKQRPQLAEGFYTGKGRVCKFCFDGGLKDWESTDEPWEHARWF 174
QY 61 PGCKYL 66
DB 175 DRCTYV 180

RESULT 16
Q6DBV7 PRELIMINARY; PRT; 322 AA.
ID Q6DBV7
AC Q6DBV7;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC078344; AAH78344.1;
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR Interpro: IPR001370; Prot_inh_132_IAP.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PSS0143; BIR_REPEAT_2; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 322 AA; 36412 MW; P9562546FA200CDF CRC64;
 Query Match 55.5%; Score 216; DB 2; Length 322;
 Best Local Similarity 53.0%; Pred. No. 7.5e-17;
 Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPMWQHAKWY 60
 DB 229 FEGRLDSFKQRHPIPERLARAGFYSTGEQDRVWCFRCGGYVAMWPDDEPMEEHARHY 288
 QY 61 PGCKYL 66
 DB 289 PGCSFL 294
 RESULT 17
 O8UWH2 PRELIMINARY; PRT; 405 AA.
 AC O8UWH2;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Xlap.
 GN Name=birc4;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;

RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 RT zebrafish."
 RL Cell Death Differ. 7:509-510(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: AF439767; AAJ32047.1; -.
 DR HSSP: P98170; 1130.
 DR ZFIN: ZDB-GENE-030825-7; birc4.
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006916; P:anti-apoptosis; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PSS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PSS0089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;
 Query Match 55.5%; Score 216; DB 2; Length 405;
 Best Local Similarity 53.0%; Pred. No. 9.5e-17;
 Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 YEARIFTGWTIVSVNKEQLARAGFYALGEGDKVCFHCGGLTDMKPSDPMWQHAKWY 60
 DB 229 FEGRLDSFKQRHPIPERLARAGFYSTGEQDRVWCFRCGGYVAMWPDDEPMEEHARHY 288
 QY 61 PGCKYL 66
 DB 289 PGCSFL 294
 RESULT 18
 Q7SKX1 PRELIMINARY; PRT; 415 AA.
 AC Q7SKX1;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Birc4 protein (Fragment).
 GN Name=birc4;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Straubeberg R.;
CL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL 1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: BC055246; AAH55246.1; -.
DR HSSP: P98170; 1130.
DR ZFIN: ZDB-GENE-030825-7; birc4.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; F:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
FT NON TER 1 1
SQ SEQUENCE 415 AA; 46788 MW; D9B82E448ADDC92 CRC64;

Query Match 55.5%; Score 216; DB 2; Length 415;
Best Local Similarity 53.0%; Pred. No. 9,7e-17;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY 1 YEARIFPTGWTIVSVNKEQARAGFYALGSGDKYKCFHCGGGLTDMKPSDPMEQNAKMY 60
DB 240 PEGRLDSFKRGQHPIDPRLARAGFYTGEDRWMCRCGGYKAMPDDEPMEHARHY 299
QY 61 PGCKYL 66
DB 300 PGCSFL 305

RESULT 19
Q6E7G7 PRELIMINARY; PRT; 287 AA.
AC 06E7G7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE IAP-3.
OS Anticarsia gemmatilis nuclear polyhedrosis virus (AgMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=31507;
RN [1]
RP SEQUENCE FROM N.A.
RA Carpes M.P., Castro M.E., Soares E.F., Villela A.G., Pinedo F.J.,
RL Ribeiro B.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY525121; AAS92269.1; -
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; F:anti-apoptosis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; Prot_inh_132_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.

SQ SEQUENCE 287 AA; 32620 MW; 20F3A7F0C11C4C2B CRC64;
Query Match 54.2%; Score 211; DB 2; Length 287;
Best Local Similarity 53.0%; Pred. No. 2.6e-16;
Matches 35; Conservative 13; Mismatches 16; Indels 2; Gaps 1;
QY 3 ARIFPTGWTIVSVNKEQARAGFYALGSGDKYKCFHCGGGLTDMKPSDPMEQNAKMY 60
DB 127 ARKTEEDWPLSKORPEQLAEAGFYTGKDKYKCFCDGGLKDWANADPEMEHARWF 186
QY 61 PGCKYL 66
DB 187 DRCSFV 192

RESULT 20
BIR3 HUMAN STANDARD; PRT; 604 AA.
ID BIR3_HUMAN
AC Q13489; Q16628; Q9HC27; Q9UP46;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 1) (HIAP1) (IAP homolog C) (Apoptosis inhibitor 2) (AIP2).
DE protein 1) (HIAP1) (IAP homolog C) (Apoptosis inhibitor 2) (AIP2).
GN Name=BIRC3; Synonyms=API2, IAP1, MICH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191; DOI=10.1038/379349a0;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,
RA Farahan R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by Nalp and a related
RT family of IAP genes.";
RL Nature 379:349-353 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514; DOI=10.1073/pnas.93.10.4974;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes.";
RL Blood 93:3418-3431 (1999).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonald M.F., Cavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.T., Skalske U., Smallus D.E.,
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RA DOI=10.1002/1098-2264(2000)999:999<:AID-GCCT1036>3.0.CO;2-I;
RA Baens M., Steyels A., Diehlamm J., De Wolf-Peters C., Marynen P.,
RT "Structure of the MALT gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type.";
RL Genes Chromosomes Cancer 29:281-291 (2000).
CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form an heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS55; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Highly expressed in fetal lung, and kidney. In
CC the adult, expression is mainly seen in lymphoid tissues.
CC -1- Including spleen, thymus and peripheral blood lymphocytes.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC3.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW=ftp://www.intoblogen.fr/services/chromocancer/Genes/BIRC3ID239.html".
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: LA9432; AAC41943.1; -;
CC EMBL: U45878; AAC50371.1; -;
CC EMBL: U37546; AAC50507.1; -;
CC EMBL: AF070674; AAC83232.1; -;
CC EMBL: BC037420; AAC37420.1; -;
CC EMBL: AF178945; AAC09369.1; -;
CC PIR: S68449; S68449.
CC HSSP: Q13490; IOBH.
CC Genew: HGNC:591; BIRC3.
CC MIM: 601721.
CC GO: GO:0005515; F:protein binding; NAS.
CC GO: GO:0006916; P:anti-apoptosis; TAS.
CC GO: GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR01029; DEATH like.
CC InterPro: IPR001841; ZnF_fing.
CC Pfam: PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50143; BIR_REPEAT_3; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS50089; zf_RING_2; 1.
KW Apoptosis; Chromosomal translocation; Repeat; zinc-finger.
FT REPEAT 29
FT REPEAT 169
FT REPEAT 255
FT DOMAIN 439
FT ZN_FING 557
FT SITE 442
FT 443
FT 18
FT 119
FT 153
FT 163
FT 165
FT 191
FT 191
FT 364
FT 552
FT 552
SQ SEQUENCE 604 AA; 68371 MW; 8581A0BA9AABA47 CRC64;
Query Match 54.2%; Score 211; DB 1; Length 604;
Best Local Similarity 57.4%; Pred. No. 5,4e-16;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY 1 YEARIFPGTWIS--VNKEQLARAGFYALGEGDKVYCFHGGGLPTDKPSEDPWEQAK 58
Db 255 HAARFKTFMFSSVVLNPEQLASAGFTYVGNSDVDKFCDCDGLRCWESGDPPVGHAK 314
QY 59 WYPCCKYL 66
Db 315 WPPRCETL 322
RESULT 21
PIAP_PIG STANDARD; PRT; 358 AA.
AC 062610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative inhibitor of apoptosis.
GN Name=PIAP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA MEDLINE=98162622; PubMed=9501011; DOI=10.1006/birc.1998.8185;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.,
RT "Cytokine induced expression of porcine inhibitor of apoptosis protein
RT (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832 (1998).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 2 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@lsb-sib.ch.

CC -----

DR EMBL, U79142; AAC39171.1; -.

DR PIR; JCS964; JCS964.

DR HSP; Q13490; IOBH.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR011029; DEATH_1like.

DR InterPro; IPR001841; Znf_fing.

DR Pfam; PF00653; BIR; 2.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 2.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS50143; BIR_REPEAT_2; 2.

DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS50518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS50089; ZF_RING_2; 1.

DR Apoptosis; Repeat; Zinc-finger.

FT REPEAT 4 70 BIR 1.

FT REPEAT 90 157 BIR 2.

FT DOMAIN 193 283 CARD.

FT ZN_FING 311 346 RING-type.

SO SEQUENCE 358 AA; 40977 MW; EB2258FA9A6190A4 CRC64;

Query Match 53.7%; Score 209; DB 1; Length 358;
Best Local Similarity 55.9%; Pred. No. 5.5e-16;
Matches 38; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARIFFGFWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTWMKSEDEPWQHAK 58
Db 90 YAAAFKTKFCWPPSSIPVHPQLASAGFYTGHSDDVRCFCDDGLRCWESGDDPWVHAK 149

Qy 59 WYPCCKYL 66
Db 150 WPPRCETYL 157

RESULT 22

Q9ESB9 PRELIMINARY; PRT; 602 AA.

AC Q9ESB9;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Inhibitor of apoptosis protein 1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=11860601;

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the Inhibitor
of Apoptosis protein 1, 2, and 3 genes.";

RL BMC Genomics 3:5-5(2002).

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.

DR EMBL; AF183430; AGG22970.1; -.

DR HSP; Q13490; IOBH.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0004942; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008370; F:zinc ion binding; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR GO; GO:0042281; P:regulation of apoptosis; IEA.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR011029; DEATH_1like.

DR InterPro; IPR001370; Prot_inh_132_IAP.

DR InterPro; IPR001841; Znf_fing.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS50143; BIR_REPEAT_2; 3.

DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

DR Metal-binding; Zinc; Zinc-finger.

SO SEQUENCE 602 AA; 67326 MW; CC91385FEA62D5A CRC64;

Query Match 53.0%; Score 206; DB 2; Length 602;
Best Local Similarity 52.9%; Pred. No. 2.1e-15;
Matches 36; Conservative 10; Mismatches 20; Indels 2; Gaps 1;

Qy 1 YEARIFFGFWIYS--VNKEQLARAGFYALGEGDKYKCFHCGGLTWMKSEDEPWQHAK 58
Db 255 HAARVKTFTWPSALVHPQLASAGFYTGHSDDVRCFCDDGLRCWESGDDPWVHAK 314

Qy 59 WYPCCKYL 66
Db 315 WPPRCETYL 322

RESULT 23

IAP3_NPVOP STANDARD; PRT; 268 AA.

ID IAP3_NPVOP

AC P41437;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Apoptosis inhibitor 3 (IAP-3).

GN Name=IAP3; Synonyms=IAP;

OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMV).

OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.

OC NCBI_TaxID=164623;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94187094; PubMed=8139034;

RA Birnbaum M.J., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
encoding a polypeptide with Cys/His sequence motifs.";

RL J. Virol. 68:2521-2528(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97271300; PubMed=9126251; DOI=10.1006/viro.1997.8448;

RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Hatwood S.,
RA Rohmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
polyhedrosis virus genome.";

RL Virology 229:381-399(1997).

RN [3]

RP INTERACTION WITH HUMAN PDCD3.

RX PubMed=15371430; DOI=10.1074/jbc.M409623200;

RA Wilkinson J.C., Richter B.W.M., Wilkinson A.S., Birstein E.,
RA Rumble J.M., Balliu B., Duckett C.S.;
RT "VIAP: a conserved inhibitor of apoptosis (IAP) interacting factor
that modulates caspase activation.";

RL J. Biol. Chem. 279:0-0(2004).

CC -1- FUNCTION: Acts by blocking cellular apoptosis rather than by
preventing viral stimulation of apoptosis.

CC -1- SUBUNIT: Interacts with human PDCD3.

CC -1- SIMILARITY: Contains 2 BIR repeats.

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC -----

DR EMBL: L22564; AAC02610.1; -.

DR EMBL: U75930; AAC59034.1; -.

DR PIR: A53989; A53989.

DR HSSP: Q24306; IUD4.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; Znf_r1ng.

DR Pfam: PF00653; BIR: 2.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR: 2.

DR SMART: SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS50143; BIR_REPEAT_2; 2.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS50089; ZF_RING_2; 1.

DR Apoptosis; Repeat; Zinc-finger.

FT REPEAT 18 84 BIR 1.

FT REPEAT 111 178 BIR 2.

FT ZN FING 221 256 RING-type.

SO SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;

Query Match 52.7%; Score 205; DB 1; Length 268;
Best Local Similarity 50.0%; Pred. No. 1.2e-15;
Matches 33; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

Qy 3 ARIFFTGWTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAQWY 60
Db 113 ARLRTPFMRGRLKQRPBELAENGFYTGQGDTRCCDGLKDMWEPDPAFMOQHAKWY 172
Qy 61 PGCKYTL 66
Db 173 DRCEYV 178

RESULT 24

Q91A70 PRELIMINARY; PRT; 195 AA.

AC Q91A70;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Inhibitor of apoptosis 1 (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC STRAIN=breed leghorn; TISSUE=Spleen;

RX MEDLINE=21158006; PubMed=11261557;

RA Zhou H., Liu W., Lamont S.J.;

RT "Genetic variation among chicken lines and mammalian species in specific genes."

RL Poul. Sci. 80:284-288(2001).

EMBL: AF221082; AAF35319.1; -.

DR HSSP: Q13490; IOBH.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro: IPR001370; Prot_inh_132_IAP.

DR Pfam: PF00653; BIR: 2.

DR SMART: SM00238; BIR: 2.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS50143; BIR_REPEAT_2; 2.

FT NON_TER 1 195

FT NON_TER 195 195

SO SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 52.4%; Score 204; DB 2; Length 195;
Best Local Similarity 54.4%; Pred. No. 1.1e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARIFFTGWTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAQWY 58
Db 116 HEARVKTFTINWPRIPRIPOVEQQLADAGFYVYGRNDVVKCFCCDGLRCWESGDDPWEIHAQ 175
Qy 59 WYPCCKYL 66
Db 176 WFPRCYVL 183

RESULT 25

Q91A69 PRELIMINARY; PRT; 197 AA.

AC Q91A69;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Inhibitor of apoptosis 1 (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC STRAIN=breed Fayoumi; TISSUE=Spleen;

RX MEDLINE=21158006; PubMed=11261557;

RA Zhou H., Liu W., Lamont S.J.;

RT "Genetic variation among chicken lines and mammalian species in specific genes."

RL Poul. Sci. 80:284-288(2001).

EMBL: AF221083; AAF35320.1; -.

DR HSSP: Q13490; IOBH.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro: IPR001370; Prot_inh_132_IAP.

DR Pfam: PF00653; BIR: 2.

DR SMART: SM00238; BIR: 2.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.

DR PROSITE; PS50143; BIR_REPEAT_2; 2.

FT NON_TER 1 197

FT NON_TER 197 197

SO SEQUENCE 197 AA; 22602 MW; D7923DABCF62351A CRC64;

Query Match 54.4%; Score 204; DB 2; Length 197;
Best Local Similarity 54.4%; Pred. No. 1.2e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARIFFTGWTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDMKPSDDPWEQHAQ 58
Db 117 HEARVKTFTINWPRIPRIPOVEQQLADAGFYVYGRNDVVKCFCCDGLRCWESGDDPWEIHAQ 176
Qy 59 WYPCCKYL 66
Db 177 WFPRCYVL 184

RESULT 26

BIR_CHICK STANDARD; PRT; 611 AA.

AC Q90660; O57319;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis protein).

GN Name=ITA; Synonyms=IAP1;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RN [1]


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Db          175 FDKCLFL 181

RESULT 28
Q921NO      PRELIMINARY;      PRT;      374 AA.
ID 0921NO
AC 0921NO
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Birc3 protein.
GN Birc3; Birc3; Synonyms=Birc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
[1]

SEQUENCE FROM N.A.
RP STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carrinci P., Prange C.,
RA Rea S.S., Loquiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Beah S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Mowley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

SEQUENCE FROM N.A.
RP STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011338; AAH1338.1; -
DR HSSP; Q13490; IQBH.
DR MGD; MGI:1197007; Birc3.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7B46F3 CRC64;

Query Match 52.2%; Score 203; DB 15; Length 374;
Best Local Similarity 52.9%; Pred. No. 2.9e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Qy          59 WYPCKYL 66
Db          313 WFPKCYL 320

RESULT 29
BIR3_MOUSE STANDARD; PRT; 600 AA.
ID BIR3_MOUSE
AC 008863;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis
DE protein 1) (MIA1) (MIA1-1).
GN Name=Birc3; Synonyms=Birc2, Iap1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
[1]

SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758; DOI=10.1006/geno.1997.5059;
RA Liotta P., Lefebvre C., Pong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form a heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2) (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the EMBL Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U88908; AAC53531.1; -
DR HSSP; Q13490; IQBH.
DR MGD; MGI:1197007; Birc2.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR011029; DEATH1 like.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR APOPTOSIS; Repeat; zinc-finger.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN FING 553 588 RING-type.
SQ SEQUENCE 600 AA; 67198 MW; AD7F33B6849317D1 CRC64;

Query Match 52.2%; Score 203; DB 15; Length 600;
Best Local Similarity 52.9%; Pred. No. 4.6e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Qy          59 WYPCKYL 66
Db          253 HAARIRTFSNWPSALVHSGELASAGFYTGHSDDVVCFCDDGLRCWBSGDDPWVHAHAK 312

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Db 313 WPRCEYL 320

RESULT 30
0804E2 PRELIMINARY; PRT; 616 AA.
AC 0804E2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN Name=CIAP-1;
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
NCBI_TaxId=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Praveen K., Leary J.H. III, Evans D.L., Jaso-Friedmann L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AY184377; AAC24632.1; -.
DR HSSP: Q13490; 10BH.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR011029; DEATH_1like.
DR InterPro: IPR001370; Prot inh_132_IAP.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00619; CARD_1.
DR SMART: SM00348; BIR_3.
DR SMART: SM00114; CARD_1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD_1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 616 AA; 69546 MW; D1389D915C6B256 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 616;
Best Local Similarity 52.2%; Pred. No. 6.2e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARLFTFGTW--LYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDEPMEOHAKW 59
DB 270 EERLLTFVMPSPRIPRPDQLAKAGFYVGRNDVXCFCCDGLRCWESGDDPWEVHAKW 329
QY 60 YPGCKYL 66
DB 330 FPRCEYL 336

RESULT 31
080WD2 PRELIMINARY; PRT; 628 AA.
AC 080WD2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Iap1.
GN Name=birc3; Synonyms=iap1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Baktaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; Pubmed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AF442500; AL33679.1; -.
DR HSSP: Q13490; 10BH.
DR ZFIN: ZDB-GENE-030825-6; birc3.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00619; CARD_1.
DR SMART: SM00348; BIR_3.
DR SMART: SM00114; CARD_1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD_1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 628 AA; 70098 MW; 5B68CEBA87C8A95 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 628;
Best Local Similarity 52.2%; Pred. No. 6.3e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARLFTFGTW--LYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDEPMEOHAKW 59
DB 280 EERLLTFVMPSPRIPRPDQLAKAGFYVGRNDVXCFCCDGLRCWESGDDPWEVHAKW 339
QY 60 YPGCKYL 66
DB 340 FPRCEYL 346

RESULT 32
0770K2 PRELIMINARY; PRT; 647 AA.
AC 0770K2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=birc3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ens K.W., Valdimarsson G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AY247786; AAP04483.1; -.
DR HSSP: P98170; 1130.
DR ZFIN: ZDB-GENE-030825-6; birc3.
```

DR GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO:00005515; F:protein binding; IEA.
DR GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006916; P:anti-apoptosis; IEA.
DR GO:0016567; P:protein ubiquitination; IEA.
DR GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR01315; CARD.
DR InterPro: IPR01029; DEATH_like.
DR InterPro: IPR01370; ProtInh_I32_IAP.
DR InterPro: IPR01841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 647 AA; 72183 MW; 88DBBAFE92718FA9 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 647;
Best Local Similarity 52.2%; Pred. No. 6.5e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARFTFGTW--ITSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDWKPSSDPWEQHAKW 59
DB 299 EBRLLTFVWNPSPRPVAPDQAKAGFYVGRNDVCKFCDDGGLRCWESGDDPVWEHAKW 358
QY 60 YPGCKYL 66
DB 359 FPRCEYL 365

RESULT 33
Q6ZM93 PRELIMINARY; PRT; 654 AA.
AC Q6ZM93; (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE S1:b2:P14.6.2 (Baculoviral IAP repeat-containing 3).
GN Name1:rc3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AL627325; CAB4763.1; -
DR GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO:0005515; F:protein binding; IEA.
DR GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006916; P:anti-apoptosis; IEA.
DR GO:0016567; P:protein ubiquitination; IEA.
DR GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR001370; ProtInh_I32_IAP.
DR InterPro: IPR01841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 654 AA; 72995 MW; A12425DE41A0259 CRC64;

Query Match 51.9%; Score 202; DB 2; Length 654;
Best Local Similarity 52.2%; Pred. No. 6.6e-15;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARFTFGTW--ITSVNKEQLARAGFYALGEGDKVCKFCGCGGLTDWKPSSDPWEQHAKW 59
DB 306 EBRLLTFVWNPSPRPVAPDQAKAGFYVGRNDVCKFCDDGGLRCWESGDDPVWEHAKW 365
QY 60 YPGCKYL 66
DB 366 FPRCEYL 372

RESULT 34
Q8IS31 PRELIMINARY; PRT; 346 AA.
ID Q8IS31;
AC Q8IS31;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxId=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY155274; AAN46550.1; -
DR HSSP: Q24306; 104Q.
DR GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006916; P:anti-apoptosis; IEA.
DR GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001370; ProtInh_I32_IAP.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A8486 CRC64;

Query Match 51.2%; Score 199; DB 2; Length 346;
Best Local Similarity 50.0%; Pred. No. 7.8e-15;
Matches 33; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIFTFGTWISVNK--EQIARAGFYALGEGDKVCKFCGCGGLTDWKPSSDPWEQHAKW 60
DB 184 ARIATFDWPRCKRQKREBLAAGFYVYGQDKTKCFYCDGGLKDWESDDVPWEHARWF 243
QY 61 PGCKYL 66
DB 244 DRCAVY 249

RESULT 35
Q968T8 PRELIMINARY; PRT; 346 AA.
ID Q968T8;
AC Q968T8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)

```
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, last annotation update)
DI Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
RN NCBI_TaxID=7091;
RP SEQUENCE FROM N.A.
RX MEDLINE=21240184; PubMed=11341966; DOI=10.1016/S0167-4889(00)00105-1;
RA Huang Q., Devereux Q.L., Maeda S., Stenicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) from Bombyx mori."
RL Biochim. Biophys. Acta 1499:191-198(2001).
DR EMBL; AF281073; AKS57560.1; -.
DR HSPB; Q24306; I04Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR01370; Prot_inh_132_IAP.
DR InterPro; IPR01841; Znf_fing.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CF6C6468894C69 CRC64;

Query Match 51.2%; Score 199; DB 2; Length 346;
Best Local Similarity 50.0%; Pred. No. 7,8e-15;
Matches 33; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIFFTGWTIVSVNK--EQIARAGFYALGEGDKYKCFHGGGLTDMKPSDPMWEOHAKWY 60
DB 184 ARATFPMDFMRBMQKPEBELAAGFFYTCGCDKCKCYCGGLDWDSDVPMQGHARWF 243
QY 61 PGCKYKL 66
DB 244 DRCAVY 249

RESULT 36
Q9ESB8 PRELIMINARY; PRT; 589 AA.
AC Q9ESB8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RX PubMed=11860601;
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the rat homologues of the inhibitor
RT of Apoptosis protein 1, 2, and 3 genes."
RL BMC Genomics 3:5-5(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF183431; AAG22971.1; -.
DR HSPB; Q13490; I0BH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
```

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DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0025981; P:regulation of apoptosis; IEA.
DR InterPro; IPR01315; CARD.
DR InterPro; IPR011028; DEATH_like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 50.9%; Score 198; DB 2; Length 589;
Best Local Similarity 52.9%; Pred. No. 1.7e-14;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIPTGWTIVS--VNKEQLARAGFYALGEGDKYKCFHGGGLTDMKPSDPMWEOHAK 58
DB 241 HSARMSFTLVWPSVAVQPEQLASAGFYVDNDVYKCFCCDGLRCWEPGDDPMIEHAK 300
QY 59 WYPCCKYL 66
DB 301 WPRCEPL 308

RESULT 37
Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22020585; PubMed=12023884; DOI=10.1042/BJ20011431;
RA Dong Z., Nishiyama J., Yi X., Venkatchalam M.A., Denton M., Gu S.,
RA Li S., Qiang M.;
RT "Gene promoter of apoptosis inhibitory protein IAP2: identification of
RT enhancer elements and activation by severe hypoxia."
RL Biochem. J. 364:413-421(2002).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF190020; AAF04585.1; -.
DR HSPB; Q13490; I0BH.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR01315; CARD.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
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Db      301 WPCRCEPL 308

RESULT 40
BIR2_MOUSE STANDARD; PRT; 612 AA.
ID_BIR2_MOUSE
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
protein 2) (MIAF2) (MIAF-2).
GN Name=BIRC2; Synonyms=BIRC3, Iap2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810; DOI=10.1016/0092-8674(95)90149-3;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel P.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758; DOI=10.1006/geno.1997.5059;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts
CC with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to
CC form a heteromeric complex, which is then recruited to the tumor
CC necrosis factor receptor 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, LA9433; AAC42078.1; -
DR EMBL, U88909; AAC53532.1; -
DR HSSP, Q13490; IQBH.
DR MGD, MGI:1197009; Birc3.
DR GO, GO:0005515; F:protein binding; IPI.
DR InterPro, IPR001370; BIR.
DR InterPro, IPR001315; CARD.
DR InterPro, IPR011029; DEATH_like.
DR InterPro, IPR001841; Znf_ring.
DR Pfam, PF00653; BIR; 3.
DR Pfam, PF00619; CARD; 1.
DR Pfam, PF00097; zf-C3HC4; 1.
DR SMART, SM00238; BIR; 3.
DR SMART, SM00114; CARD; 1.
DR SMART, SM00184; RING; 1.
DR PROSITE, PS01282; BIR_REPEAT_1; 3.
DR PROSITE, PS50143; BIR_REPEAT_2; 3.
DR PROSITE, PS50209; CARD; 1.

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DR PROSITE, PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE, PS50089; ZF_RING_2; 1.
KW Apoptosis; Direct protein sequencing; Repeat; Zinc-finger.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-type.
FT CONFLICT 380 380 E -> K (in Ref. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 612;
Best Local Similarity 52.9%; Pred. No. 2,4e-14;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFPGWIVS--VNKEQLARAGFYALGEGDKYKCFHGGGGLTDWKPSEDPMWROHAK 58
Db 262 HSRRLRTFLYPPSVFVQPEQLASAGFTYVDRNDVKCFCCDGLKCMERGDPMWIEHAK 321
QY 59 WYPGCKYL 66
Db 322 WPCRCEPL 329

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Search completed: June 15, 2005, 17:39:36
Job time : 113.5 secs